## SEQUENCE LISTING

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gcc gc Ala Al	a Val	aag Lys	gag Glu	att Ile	cgc Arg 55	tcc Ser	atc Ile	cga Arg	aaa Lys	tgg Trp 60	gcc Ala	tac Tyr	gag Glu	acc Thr	192
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atc gt Ile Va	cc gat al Asp 115	Val	gct Ala	gag Glu	cga Arg	gcc Ala 120	ggc Gly	gtt Val	cac His	gcc Ala	gta Val 125	tgg Trp	gct Ala	ggc	384

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tcc Ser 145	aag Lys	cac His	aag Lys	atc Ile	atc Ile 150	ttt Phe	atc Ile	ggt Gly	ccc Pro	ccc Pro 155	ggc Gly	tcc Ser	gcc Ala	atg Met	cgc Arg 160	480
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gag Glu	tcc Ser	atg Met	gag Glu	aag Lys 325	gct Ala	gcc Ala	gtg Val	cgt Arg	ctc Leu 330	Ala	aaa Lys	ctg Leu	gtt Val	ggc Gly 335	tac Tyr	1008
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ttt Phe	gcc Ala	tto Phe	Leu	gag Glu	ctc Leu	aac Asn	ccc Pro 360	Arg	ctt Leu	cag Gln	gtc Val	gag Glu 365	His	cct Pro	act Thr	1104

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Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile 35 40 45

25

20

- Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr 50 60
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- Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu 100 105 110
- Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly
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- Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp 165 170 175
- Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met 180 185 190
- Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala 195 200 205
- Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly 210 215 220
- Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile 225 230 235 240
- Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val 245 250 255
- Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly 260 265 270

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C	∄lu	Ser	Met	Glu	Lys 325	Ala	Ala	Val	Arg	Leu 330	Ala	Lys	Leu	Val	Gly 335	Tyr
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7	Val		_	_		Thr									Lys	Pro
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Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp

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	atc Ile															768	
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	ccc Pro															864	
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	tac Tyr															1056	
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	gtg Val 370															1152	
gct	gct	caa	ctg	caa	gtg	gct	atg	ggt	att	ccg	ctg	cac	tgc	atc	ccg	1200	

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gcg Ala	cgt Arg	att Ile 435	acc Thr	gcc Ala	gag Glu	gat Asp	ccg Pro 440	aac Asn	gcc Ala	ggt Gly	ttc Phe	cag Gln 445	cct Pro	acc Thr	agt Ser	1344
	gcc Ala 450															1392
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cac His	acg Thr	acg Thr 515	gtc Val	gag Glu	tac Tyr	atc Ile	gtt Val 520	aac Asn	atg Met	atg Met	gag Glu	tct Ser 525	gat Asp	gat Asp	ttc Phe	1584
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	aat Asn															1665
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Glı	ı Thr	Arg	Ser 20	Asp	Ser	Asn	Pro	Leu 25	Asn	Tyr	Ala	Ser	Met 30	Glu	Glu	
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Met	Ala	Thr	Pro	Glu 85	Asp	Leu	Lys	Ala	Asn 90	Ala	Glu	Tyr	Ile	Arg 95	Met
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Ala	Asn	Val 115	Ser	Leu	Ile	Ile	Glu 120	Ile	Ala	Glu	Arg	Phe 125	Asn	Val	Asp
Ala	Val 130	Trp	Ala	Gly	Trp	Gly 135	His	Ala	Ser	Glu	Asn 140	Pro	Leu	Leu	Pro
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Gly	Lys	Pro	Met	Arg 165	Ala	Leu	Gly	Asp	Lys 170	Ile	Gly	Ser	Thr	Ile 175	Ile
Ala	Gln	Ser	Ala 180	Lys	Val	Pro	Thr	Ile 185	Ala	Trp	Asn	Gly	Asp 190	Gly	Met
Glu	Val	Asp 195	Tyr	Lys	Glu	His	Asp 200	Gly	Ile	Pro	Asp	Glu 205	Ile	Tyr	Asn
Ala	Ala 210	Met	Leu	_	Asp	_		His	Cys		Asp 220		Cys	Lys	Arg
Ile 225	Gly	Phe	Pro	Val	Met 230	Ile	Lys	Ala	Ser	Glu 235	Gly	Gly	Gly	Gly	Lys 240
Gly	Ile	Arg	Met	Val 245	His	Glu	Glu	Ser	Gln 250	Val	Leu	Ser	Ala	Trp 255	Glu
Ala	Val	Arg	Gly 260	Glu	Ile	Pro	Gly	Ser 265	Pro	Ile	Phe	Val	Met 270	Lys	Leu
Ala	Pro	Lys 275	Ser	Arg	His	Leu	Glu 280	Val	Gln	Leu	Leu	Ala 285	Asp	Thr	Tyr

Gly Asn Ala Ile Ala Leu Ser Gly Arg Asp Cys Ser Val Gln Arg Arg 290 His Gln Lys Ile Val Glu Glu Gly Pro Val Leu Ala Pro Thr Gln Glu 310 Val Trp Glu Lys Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val 330 325 Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro 345 Glu Asp Asn Gly Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu 360 Gln Val Glu His Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro 375 Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro 390 395 Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile 410 Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala 420 Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly 455 Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser 470 465 Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg 485 490 Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile 505 500 His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe

520

515

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gct gcc Ala Ala															288
ttc gga Phe Gly															336
gat ttg Asp Leu		_		_	-			_	_	_	_				384
gag gtc Glu Val 130	Pro														432
atc gtc Ile Val 145	-	_			_	_				_	-		-		480
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														cct Pro		1200
														cag Gln		1248

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	c aag ctc tcg act ga o Lys Leu Ser Thr G 440		
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	c atg cac gag ctg as L Met His Glu Leu As 485		
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Asp 65	Gly	His	Thr	Val	Ile 70	Thr	Asn	Val	Leu	Ile 75	Ala	Asn	Asn	Gly	Ile 80
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Phe	Gly	Asp	Glu 100	Arg	Ala	Ile	Gln	Phe 105	Thr	Val	Met	Ala	Thr 110	Pro	Glu
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Glu	Val 130	Pro	Gly	Gly	Thr	Asn 135	Asn	Asn	Asn	Tyr	Ala 140	Asn	Val	Glu	Leu
Ile 145	Val	Asp	Val	Ala	Glu 150	Arg	Met	Asn	Val	His 155	Ala	Val	Trp	Ala	Gly 160
Trp	Gly	His	Ala	Ser 165	Glu	Asn	Pro	Lys	Leu 170	Pro	Glu	Ser	Leu	Ala 175	Ala
Ser	Pro	Lys	Lys 180	Ile	Ile	Phe	Ile	Gly 185	Pro	Pro	Gly	Ser	Ala 190	Met	Arg
Ser	Leu	Gly 195	Asp	Lys	Ile	Ser	Ser 200	Thr	Ile	Val	Ala	Gln 205	His	Ala	Gln
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Cys	Val	Thr	Ser	Trp 245	Gln	Glu	Gly	Leu	Glu 250	Lys	Ala	Arg	Gln	Ile 255	Gly
Phe	Pro	Val	Met 260	Ile	Lys	Ala	Ser	Glu 265	Gly	Gly	Gly	Gly	Lys 270	Gly	Ile

Arg	Lys	A1a 275	Val	Ser	GIU	GIu	280	Pne	Glu	Glu	Leu	1yr 285	гÀг	Ala	Ala
Ala	Ser 290	Glu	Ile	Pro	Gly	Ser 295	Pro	Ile	Phe	Ile	Met 300		Leu	Ala	Gly
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Asn	Ile	Ser	Leu	Phe 325	Gly	Arg	Asp	Cys	Ser 330	Val	Gln	Arg	Arg	His 335	Gln
Lys	Ile	Ile	Glu 340	Glu	Ala	Pro	Val	Thr 345	Ile	Ala	Lys	Pro	Asp 350	Thr	Phe
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Gly	Val	Asp 435	Pro	Lys	Leu	Ser	Thr 440	Glu	Ile	Asp	Phe	Asp 445	Phe	Lys	Asn
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Asp Phe Arg Thr Thr Val Glu Tyr 1 545 550	Leu Ile Lys Leu Leu Glu Thr Glu 555 560
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<222> (226)(228) <223> Alteration of Ser-77 codo	ing  tot coa cag aag atg gag tac gaa 48
<222> (226)(228)  <223> Alteration of Ser-77 codo eliminates soraphen bindi  <400> 7 tct gaa gaa agc tta ttc gag tct Ser Glu Glu Ser Leu Phe Glu Ser 1 5  att aca aac tac tca gaa aga cat Ile Thr Asn Tyr Ser Glu Arg His	tct cca cag aag atg gag tac gaa 48 Ser Pro Gln Lys Met Glu Tyr Glu 10 15 aca gaa ctt cca ggt cat ttc att 96
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<pre>&lt;222&gt; (226)(228) &lt;223&gt; Alteration of Ser-77 codo         eliminates soraphen bindi  &lt;400&gt; 7 tct gaa gaa agc tta ttc gag tct Ser Glu Glu Ser Leu Phe Glu Ser 1</pre>	tct cca cag aag atg gag tac gaa 48 Ser Pro Gln Lys Met Glu Tyr Glu 10 15  aca gaa ctt cca ggt cat ttc att 96 Thr Glu Leu Pro Gly His Phe Ile 25 30  gag gag tcc ccg tta agg gac ttt Glu Glu Ser Pro Leu Arg Asp Phe 45  gtc ata tcc aag atc ctg ata gca 192
<pre>&lt;222&gt; (226)(228) &lt;223&gt; Alteration of Ser-77 codo         eliminates soraphen bindi  &lt;400&gt; 7 tct gaa gaa agc tta ttc gag tct Ser Glu Glu Ser Leu Phe Glu Ser 1</pre>	tct cca cag aag atg gag tac gaa 48  Ser Pro Gln Lys Met Glu Tyr Glu 10 15  aca gaa ctt cca ggt cat ttc att 96  Thr Glu Leu Pro Gly His Phe Ile 25 30  gag gag tcc ccg tta agg gac ttt Glu Glu Ser Pro Leu Arg Asp Phe 45  gtc ata tcc aag atc ctg ata gca Val Ile Ser Lys Ile Leu Ile Ala 60  gaa att aga tcc gtc aga aaa tgg 240

gcc Ala	acc Thr	cca Pro	gaa Glu 100	gat Asp	ctg Leu	gag Glu	gcc Ala	aac Asn 105	gca Ala	gaa Glu	tat Tyr	atc Ile	cgt Arg 110	atg Met	gcc Ala	336
					gtg Val											384
					gta Val											432
gta Val 145	tgg Trp	gct Ala	ggc Gly	tgg Trp	ggt Gly 150	cac His	gcc Ala	tcc Ser	gag Glu	aat Asn 155	cca Pro	cta Leu	ttg Leu	cct Pro	gaa Glu 160	480
					aag Lys											528
					tta Leu											576
					cca Pro											624
					gag Glu											672
					tgt Cys 230											720
					ttt Phe											768
ggt Gly	ggt Gly	aaa Lys	ggt Gly 260	atc Ile	aga Arg	caa Gln	gtt Val	gaa Glu 265	cgt Arg	gaa Glu	gaa Glu	gat Asp	ttc Phe 270	atc Ile	gct Ala	816
tta Leu	tac Tyr	cac His 275	cag Gln	gca Ala	gcc Ala	aac Asn	gaa Glu 280	att Ile	cca Pro	ggc Gly	tcc Ser	ccc Pro 285	att Ile	ttc Phe	atc Ile	864
atg Met	aag Lys 290	ttg Leu	gcc Ala	ggt Gly	aga Arg	gcg Ala 295	cgt Arg	cac His	ttg Leu	gaa Glu	gtt Val 300	caa Gln	ctg Leu	cta Leu	gca Ala	912
gat Asp 305	cag Gln	tac Tyr	ggt Gly	aca Thr	aat Asn 310	att Ile	tcc Ser	ttg Leu	ttc Phe	ggt Gly 315	aga Arg	gac Asp	tgt Cys	tcc Ser	gtt Val 320	960
cag Gln	aga Arg	cgt Arg	cat His	caa Gln 325	aaa Lys	att Ile	atc Ile	gaa Glu	gaa Glu 330	gca Ala	cca Pro	gtt Val	aca Thr	att Ile 335	gcc Ala	1008
aag	gct	gaa	aca	ttt	cac	gag	atg	gaa	aag	gct	gcc	gtc	aga	ctg	aaa	1056

Lys	Ala	Glu	Thr 340	Phe	His	Glu	Met	Glu 345	Lys	Ala	Ala	Val	Arg 350	Leu	Gly	
											gag Glu					1104
cat His	gat Asp 370	gat Asp	gga Gly	aaa Lys	ttc Phe	tac Tyr 375	ttt Phe	tta Leu	gaa Glu	ttg Leu	aac Asn 380	cca Pro	aga Arg	tta Leu	caa Gln	1152
gtc Val 385	gag Glu	cat His	cca Pro	aca Thr	acg Thr 390	gaa Glu	atg Met	gtc Val	tcc Ser	ggt Gly 395	gtt Val	aac Asn	tta Leu	cct Pro	gca Ala 400	1200
gct Ala	caa Gln	tta Leu	caa Gln	atc Ile 405	gct Ala	atg Met	ggt Gly	atc Ile	cct Pro 410	atg Met	cat His	aga Arg	ata Ile	agt Ser 415	gac Asp	1248
att Ile	aga Arg	act Thr	tta Leu 420	tat Tyr	ggt Gly	atg Met	aat Asn	cct Pro 425	cat His	tct Ser	gcc Ala	tca Ser	gaa Glu 430	atc Ile	gat Asp	1296
ttc Phe	gaa Glu	ttc Phe 435	aaa Lys	act Thr	caa Gln	gat Asp	gcc Ala 440	acc Thr	aag Lys	aaa Lys	caa Gln	aga Arg 445	aga Arg	cct Pro	att Ile	1344
cca Pro	aag Lys 450	ggt Gly	cat His	tgt Cys	acc Thr	gct Ala 455	tgt Cys	cgt Arg	atc Ile	aca Thr	tca Ser 460	gaa Glu	gat Asp	cca Pro	aac Asn	1392
gat Asp 465	gga Gly	ttc Phe	aag Lys	cca Pro	tcg Ser 470	ggt Gly	ggt Gly	act Thr	ttg Leu	cat His 475	gaa Glu	cta Leu	aac Asn	ttc Phe	cgt Arg 480	1440
tct Ser	tcc Ser	tct Ser	aat Asn	gtt Val 485	tgg Trp	ggt Gly	tac Tyr	ttc Phe	tcc Ser 490	gtg Val	ggt Gly	aac Asn	aat Asn	ggt Gly 495	aat Asn	1488
att Ile	cac His	tcc Ser	ttt Phe 500	tcg Ser	gac Asp	tct Ser	cag Gln	ttc Phe 505	ggc	cat His	att Ile	ttt Phe	gct Ala 510	ttt Phe	ggt Gly	1536
gaa Glu	aat Asn	aga Arg 515	Gln	gct Ala	tcc Ser	agg Arg	aaa Lys 520	cac His	atg Met	gtt Val	gtt Val	gcc Ala 525	ctg Leu	aag Lys	gaa Glu	1584
ttg Leu	tcc Ser 530	Ile	agg Arg	ggt Gly	gat Asp	ttc Phe 535	Arg	act Thr	act Thr	gtg Val	gaa Glu 540	tac Tyr	ttg Leu	atc Ile	aaa Lys	1632
ctt Leu 545	Leu	gaa Glu	act Thr	gaa Glu	gat Asp 550	ttc Phe	gag Glu	gat Asp	aac Asn	act Thr 555	att Ile	acc Thr	acc Thr	ggt Gly	tgg Trp 560	1680
ttg Leu	gac Asp	gat Asp	ttg Leu	att Ile 565	Thr	cat His	aaa Lys	atg Met	acc Thr 570	Ala	gaa Glu	aag Lys	cct Pro	gat Asp 575	cca Pro	1728
		_	gtc Val													1740

			580				
<211 <212	)> { L> ! 2> ] 3> \$	580	naron	nyces	s cei	revis	siae
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Ile	Thr	Asn	Tyr 20	Ser	Glu	Arg	His
∃ly	Leu	Asn 35	Thr	Val	Asp	Lys	Leu 40
/al	Lys 50	Ser	His	Gly	Gly	His 55	Thr
Asn 55	Asn	Gly	Ile	Ala	Ala 70	Val	Lys
		_			_		

- Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu 1 . 5 10 15
- Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile 20 25 30
- Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe 35 40 45
- Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 50 55 60
- Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp 65 70 75 80
- Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met 85 90 95
- Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala 115 120 125
- Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala 130 135 140
- Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu 145 150 155 160
- Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly 165 170 175
- Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala 180 185 190
- Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp 195 200 205

Thr	Val 210	His	Val	Asp	Glu	Lys 215	Thr	Gly	Leu	Val	Ser 220	Val	Asp	Asp	Asp
Ile 225	Tyr	Gln	Lys	Gly	Cys 230	Cys	Thr	Ser	Pro	Glu 235	Asp	Gly	Leu	Gln	Lys 240
Ala	Lys	Arg	Ile	Gly 245	Phe	Pro	Val	Met	Ile 250	Lys	Ala	Ser	Glu	Gly 255	Gly
Gly	Gly	Lys	Gly 260	Ile	Arg	Gln	Val	Glu 265	Arg	Glu	Glu	Asp	Phe 270	Ile	Ala
Leu	Tyr	His 275	Gln	Ala	Ala	Asn	Glu 280	Ile	Pro	Gly	Ser	Pro 285	Ile	Phe	Ile
Met	Lys 290	Leu	Ala	Gly	Arg	Ala 295	Arg	His	Leu	Glu	Val 300	Gln	Leu	Leu	Ala
Asp 305	Gln	Tyr	Gly	Thr	Asn 310	Ile	Ser	Leu	Phe	Gly 315	Arg	Asp	Cys	Ser	Val 320
Gln	Arg	Arg	His	Gln 325	Lys	Ile	Ile	Glu	Glu 330	Ala	Pro	Val	Thr	Ile 335	Ala
Lys	Ala	Glu	Thr 340	Phe	His	Glu	Met	Glu 345	Lys	Ala	Ala	Val	Arg 350	Leu	Gly
Lys	Leu	Val 355	Gly	Tyr	Val	Ser	Ala 360	Gly	Thr	Val	Glu	Tyr 365	Leu	Tyr	Ser
His	Asp 370	Asp	Gly	Lys	Phe	Tyr 375	Phe	Leu	Glu	Leu	Asn 380	Pro	Arg	Leu	Gln
Val 385	Glu	His	Pro	Thr	Thr 390	Glu	Met	Val	Ser	Gly 395	Val	Asn	Leu	Pro	Ala 400
Ala	Gln	Leu	Gln	Ile 405	Ala	Met	Gly	Ile	Pro 410	Met	His	Arg	Ile	Ser 415	Asp
Ile	Arg	Thr	Leu 420	Tyr	Gly	Met	Asn	Pro 425	His	Ser	Ala	Ser	Glu 430	Ile	Asp
Phe	Glu	Phe 435	Lys	Thr	Gln	Asp	Ala 440	Thr	Lys	Lys	Gln	Arg 445	Arg	Pro	Ile

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn 450 455 460	
Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg 465 470 475 480	
Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn 485 490 495	
Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly 500 505 510	
Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu 515 520 525	
Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 530 535 540	
Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp 545 550 555 560	
Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro 565 570 575	
Thr Leu Ala Val	
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<220> <221> CDS <222> (1)(1896) <223> Human ACCasel (alpha) BC domain (aa 1-632)	
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tct cga ttc ata ata ggt tct gtg tct gaa gat aac tca gag gat gag Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu 20 25 30	96
atc agc aac ctg gtg aag ttg gac cta ctg gag gag aag gag ggc tcc Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser 35 40 45	144
ttg tca cct gct tct gtt ggc tca gat aca ctc tct gat ttg ggg atc	192

Leu	Ser 50	Pro	Ala	Ser	Val	Gly 55	Ser	Asp	Thr	Leu	Ser 60	Asp	Leu	Gly	Ile		
tct Ser 65	agc Ser	cta Leu	cag Gln	gat Asp	ggc Gly 70	ttg Leu	gcc Ala	ttg Leu	cac His	ata Ile 75	agg Arg	tcc Ser	agc Ser	atg Met	tct Ser 80	2	240
														gat Asp 95		2	288
caa Gln	cga Arg	gat Asp	ttc Phe 100	act Thr	gtg Val	gct Ala	tct Ser	cca Pro 105	gca Ala	gaa Glu	ttt Phe	gtt Val	act Thr 110	cgc Arg	ttt Phe	:	336
Gly 999	gga Gly	aat Asn 115	aaa Lys	gtg Val	att Ile	gag Glu	aag Lys 120	gtt Val	ctt Leu	att Ile	gct Ala	aac Asn 125	aat Asn	ggc Gly	att Ile	;	384
														gaa Glu		•	432
ttt Phe 145	cga Arg	aat Asn	gaa Glu	cgt Arg	gca Ala 150	att Ile	aga Arg	ttc Phe	gtt Val	gtc Val 155	atg Met	gtc Val	aca Thr	cct Pro	gaa Glu 160		480
														tat Tyr 175			528
cca Pro	gtg Val	cct Pro	gga Gly 180	gga Gly	cca Pro	aac Asn	aac Asn	aac Asn 185	aac Asn	tat Tyr	gca Ala	aat Asn	gtg Val 190	gaa Glu	tta Leu		576
att Ile	ctt Leu	gat Asp 195	att Ile	gct Ala	aaa Lys	agg Arg	atc Ile 200	cca Pro	gtg Val	cag Gln	gca Ala	gtg Val 205	tgg Trp	gct Ala	ggc Gly		624
												Leu		ttg Leu			672
														gct Ala			720
Gly 333	gat Asp	aag Lys	att Ile	gca Ala 245	tct Ser	tcc Ser	ata Ile	gtg Val	gct Ala 250	caa Gln	act Thr	gca Ala	ggt Gly	atc Ile 255	cca Pro		768
act Thr	ctt Leu	ccc Pro	tgg Trp 260	agc Ser	ggc	agt Ser	ggt Gly	ctt Leu 265	cgt Arg	gtg Val	gac Asp	tgg Trp	cag Gln 270	gaa Glu	aat Asn		816
gat Asp	ttt Phe	tca Ser 275	Lys	cgt Arg	atc Ile	tta Leu	aat Asn 280	gtt Val	ccc Pro	cag Gln	gag Glu	cta Leu 285	tat Tyr	gaa Glu	aaa Lys		864
ggt Gly	tat Tyr	gtg Val	aaa Lys	gat Asp	gtg Val	gat Asp	gat Asp	gly aaa	cta Leu	aag Lys	gca Ala	gct Ala	gag Glu	gaa Glu	gtt Val		912

290	295	300

						tca Ser								960
	_	_		-	_	gac Asp						_	_	1008
						ccc Pro 345								1056
						cag Gln								1104
						gat Asp								1152
						gct Ala								1200
						gtg Val								1248
						tac Tyr 425								1296
						cgg Arg								1344
						ctc Leu								1392
_	_				_	atc Ile	_	_		_	_	_		1440
						ccc Pro								1488
	_	_		 		gtt Val 505		_	_				_	1536
_		_			_	ccc Pro	-				-	_		1584
		_	_	_		gtt Val					_	-	_	1632

Ala Ala Gly 545	gga ctt Gly Leu									1680
ttt tct tgg Phe Ser Trp	gga gaa Gly Glu 565	aac aga Asn Arg	gaa ga Glu Gl	ag gca Lu Ala 570	att to Ile Se	ca aac er Asn	atg Met	gtg Val 575	gtg Val	1728
gct ttg aag Ala Leu Lys				y Asp						1776
tac ctg atc Tyr Leu Ile 595										1824
gat act ggc Asp Thr Gly 610			Leu Il		Glu L					1872
cga cct gac Arg Pro Asp 625	_		_							1896
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Met Asp Glu	5			10 er Glu				15		
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Met Asp Glu  1  Ser Arg Phe  Ile Ser Asn	Ile Ile 20 Leu Val	Gly Ser	Val Se 25 Asp Le 40	10 er Glu 5	Asp As	sn Ser lu Lys 45 er Asp	Glu 30 Glu	15 Asp Gly	Glu Ser	
Met Asp Glu  1  Ser Arg Phe  Ile Ser Asn 35  Leu Ser Pro	Ile Ile 20 Leu Val	Gly Ser Lys Leu Val Gly 55	Val Se 25 Asp Le 40	10 er Glu 5 eu Leu sp Thr	Asp As Glu G	sn Ser lu Lys 45 er Asp 0	Glu 30 Glu Leu	Asp Gly	Glu Ser Ile	
Met Asp Glu  1  Ser Arg Phe  Ile Ser Asn 35  Leu Ser Pro 50  Ser Ser Leu	Ile Ile 20 Leu Val Ala Ser	Gly Ser Lys Leu Val Gly 55 Gly Leu 70	Val Se 25 Asp Le 40 Ser As	10 er Glu eu Leu sp Thr	Asp As Glu G: Leu Sc 60 Ile A: 75	sn Ser lu Lys 45 er Asp 0	Glu 30 Glu Leu Ser	Asp Gly Gly Met	Glu Ser Ile Ser 80	

Gly	Gly	Asn 115	Lys	Val	Ile	Glu	Lys 120	Val	Leu	Ile	Ala	125	Asn	GIY	IIe
Ala	Ala 130	Val	Lys	Cys	Met	Arg 135	Ser	Ile	Arg	Arg	Trp 140	Ser	Tyr	Glu	Met
Phe 145	Arg	Asn	Glu	Arg	Ala 150	Ile	Arg	Phe	Val	Val 155	Met	Val	Thr	Pro	Glu 160
Asp	Leu	Lys	Ala	Asn 165	Ala	Glu	Tyr	Ile	Lys 170	Met	Ala	Asp	His	Tyr 175	Val
Pro	Val	Pro	Gly 180	Gly	Pro	Asn	Asn	Asn 185	Asn	Tyr	Ala	Asn	Val 190	Glu	Leu
Ile	Leu	Asp 195	Ile	Alá	Lys	Arg	Ile 200	Pro	Val	Gln	Ala	Val 205	Trp	Ala	Gly
Trp	Gly 210	His	Ala	Ser	Glu	Asn 215	Pro	Lys	Leu	Pro	Glu 220	Leu	Leu	Leu	Lys
Asn 225	Gly	Ile	Ala	Phe	Met 230	Gly	Pro	Pro	Ser	Gln 235	Ala	Met	Trp	Ala	Leu 240
Gly	Asp	Lys	Ile	Ala 245	Ser	Ser	Ile	Val	Ala 250	Gln	Thr	Ala	Gly	Ile 255	Pro
Thr	Leu	Pro	Trp 260	Ser	Gly	Ser	Gly	Leu 265	Arg	Val	Asp	Trp	Gln 270	Glu	Asn
Asp	Phe	Ser 275	Lys	Arg	Ile	Leu	Asn 280	Val	Pro	Gln	Glu	Leu 285	Tyr	Glu	Lys
Gly	Tyr 290	Val	Lys	Asp	Val	Asp 295	Asp	Gly	Leu	Lys	Ala 300	Ala	Glu	Glu	Val
Gly 305	Tyr	Pro	Val	Met	Ile 310	Lys	Ala	Ser	Glu	Gly 315	Gly	Gly	Gly	Lys	Gly 320
Ile	Arg	Lys	Val	Asn 325	Asn	Ala	Asp	Asp	Phe 330	Pro	Asn	Leu	Phe	Arg 335	Gln
Val	Gln	Ala	Glu 340	Val	Pro	Gly	Ser	Pro 345	Ile	Phe	Val	Met	Arg 350	Leu	Ala
Tara	Cln	Cor	7. **	uic	Tou	Glu	Val.	Gln	Tla	T 011	λΊэ	λan	Gln	ጥህን	Glv

355 360 365

Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His 370 375 380

Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val 385 390 395 400

Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly
405 410 415

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser 420 425 430

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys 435 440 445

Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile 450 455 460

Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr 465 470 475 480

Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala 485 490 495

His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser 500 505 510

Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu 515 520 525

Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala 530 540

Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys 545 550 555 560

Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val 565 570 575

Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu 580 585 590

Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile 595 600 605 Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu 610 620

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ttt Phe	tcc Ser	tgg Trp	tta Leu 20	aaa Lys	atc Ile	tgg Trp	gly ggg	aaa Lys 25	atg Met	acg Thr	gac Asp	tcc Ser	aag Lys 30	ccg Pro	atc Ile	96
acc Thr	aag Lys	agt Ser 35	aaa Lys	tca Ser	gaa Glu	gca Ala	aac Asn 40	ctc Leu	atc Ile	ccg Pro	agc Ser	cag Gln 45	gag Glu	ccc Pro	ttt Phe	144
cca Pro	gcc Ala 50	tct Ser	gat Asp	aac Asn	tca Ser	999 Gly 55	gag Glu	aca Thr	ccg Pro	cag Gln	aga Arg 60	aat Asn	gly aaa	gag Glu	ggc Gly	192
cac His 65	act Thr	ctg Leu	ccc Pro	aag Lys	aca Thr 70	ccc Pro	agc Ser	cag Gln	gcc Ala	gag Glu 75	cca Pro	gcc Ala	tcc Ser	cac His	aaa Lys 80	240
ggc Gly	ccc Pro	aaa Lys	gat Asp	gcc Ala 85	ggt Gly	cgg Arg	cgg Arg	aga Arg	aac Asn 90	tcc Ser	cta Leu	cca Pro	ccc Pro	tcc Ser 95	cac His	288
cag Gln	aag Lys	ccc Pro	cca Pro 100	aga Arg	aac Asn	ccc Pro	ctt Leu	tct Ser 105	tcc Ser	agt Ser	gac Asp	gca Ala	gca Ala 110	ccc Pro	tcc Ser	336
cca Pro	gag Glu	ctt Leu 115	caa Gln	gcc Ala	aac Asn	gly aaa	act Thr 120	gly ggg	aca Thr	caa Gln	ggt Gly	ctg Leu 125	gag Glu	gcc Ala	aca Thr	384
gat Asp	acc Thr 130	aat Asn	ggc Gly	ctg Leu	tcc Ser	tcc Ser 135	tca Ser	gcc Ala	agg Arg	ccc Pro	cag Gln 140	ggc	cag Gln	caa Gln	gct Ala	432
ggc Gly 145	tcc Ser	ccc Pro	tcc Ser	aaa Lys	gaa Glu 150	gac Asp	aag Lys	aag Lys	cag Gln	gca Ala 155	aac Asn	atc Ile	aag Lys	agg Arg	cag Gln 160	480

ctg Leu	atg Met	acc Thr	aac Asn	ttc Phe 165	atc Ile	ctg Leu	ggc Gly	tct Ser	ttt Phe 170	gat Asp	gac Asp	tac Tyr	tcc Ser	tct Ser 175	gac Asp	528
gag Glu	gac Asp	tct Ser	gtt Val 180	gct Ala	ggc Gly	tca Ser	tct Ser	cgt Arg 185	gag Glu	tct Ser	acc Thr	cgg Arg	aag Lys 190	ggc Gly	agc Ser	576
cgg Arg	gcc Ala	agc Ser 195	ttg Leu	gly aaa	gcc Ala	ctg Leu	tcc Ser 200	ctg Leu	gag Glu	gct Ala	tat Tyr	ctg Leu 205	acc Thr	aca Thr	ggt Gly	624
														gga Gly		672
cac His 225	ctg Leu	gtg Val	aag Lys	agg Arg	gga Gly 230	cgg Arg	gaa Glu	cac His	aag Lys	aag Lys 235	ctg Leu	gac Asp	ctg Leu	cac His	aga Arg 240	720
gac Asp	ttt Phe	acc Thr	gtg Val	gct Ala 245	tct Ser	ccc Pro	gct Ala	gag Glu	ttt Phe 250	gtc Val	aca Thr	cgc Arg	ttt Phe	ggg Gly 255	Gly ggg	768
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														ttc Phe		864
														gac Asp		912
														ccc Pro		960
														att Ile 335		1008
														tgg Trp		1056
cat His	gct Ala	tca Ser 355	gaa Glu	aac Asn	cct Pro	aaa Lys	ctt Leu 360	ccg Pro	gag Glu	ctg Leu	ctg Leu	tgc Cys 365	aag Lys	aat Asn	gga Gly	1104
		Phe												gga Gly		1152
	Ile													acc Thr		1200

					ggc Gly											1248
					atc Ile											1296
					gat Asp											1344
		_	_		aaa Lys	_		_								1392
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					ggc Gly											1488
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					tgt Cys 550											1680
					gtg Val											1728
					aat Asn											1776
					gtt Val											1824
					cac His											1872
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aat Asn	ttc Phe	cgg Arg 675	agc Ser	agc Ser	aag Lys	aac Asn	gtg Val 680	tgg Trp	ggt Gly	tac Tyr	ttc Phe	agc Ser 685	gtg Val	gcc Ala	gct Ala	2064
act Thr	gga Gly 690	ggc Gly	ctg Leu	cac His	gag Glu	ttt Phe 695	gcg Ala	gat Asp	tcc Ser	caa Gln	ttt Phe 700	gl <sup>à</sup> aaa	cac His	tgc Cys	ttc Phe	2112
tcc Ser 705	tgg Trp	gga Gly	gag Glu	aac Asn	cgg Arg 710	aaa Lys	gag Glu	gcc Ala	att Ile	tcg Ser 715	aac Asn	atg Met	gtg Val	gtg Val	gct Ala 720	2160
ttg Leu	aag Lys	gaa Glu	ctg Leu	tcc Ser 725	atc Ile	cga Arg	ggt Gly	gac Asp	ttt Phe 730	agg Arg	act Thr	acc Thr	gtg Val	gaa Glu 735	tac Tyr	2208
ctc Leu	att Ile	aac Asn	ctc Leu 740	ctg Leu	gag Glu	acc Thr	gag Glu	agc Ser 745	ttc Phe	cag Gln	aac Asn	aac Asn	gac Asp 750	atc Ile	gac Asp	2256
acc Thr	Gly ggg	tgg Trp 755	ttg Leu	gac Asp	tac Tyr	ctc Leu	att Ile 760	gct Ala	gag Glu	aaa Lys	gtg Val	cag Gln 765	gag Glu	aaa Lys	ccg Pro	2304
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Gly	Pro	Lys	Asp	Ala 85	Gly	Arg	Arg	Arg	Asn 90	Ser	Leu	Pro	Pro	Ser 95	His
Gln	Lys	Pro	Pro 100	Arg	Asn	Pro	Leu	Ser 105	Ser	Ser	Asp	Ala	Ala 110	Pro	Ser
Pro	Glu	Leu 115	Gln	Ala	Asn	Gly	Thr 120	Gly	Thr	Gln	Gly	Leu 125	Glu	Ala	Thr
Asp	Thr 130	Asn	Gly	Leu	Ser	Ser 135	Ser	Ala	Arg	Pro	Gln 140	Gly	Gln	Gln	Ala
Gly 145	Ser	Pro	Ser	Lys	Glu 150	Asp	Lys	Lys	Gln	Ala 155	Asn	Ile	Lys	Arg	Gln 160
Leu	Met	Thr	Asn	Phe 165	Ile	Leu	Gly	Ser	Phe 170	Asp	Asp	Tyr	Ser	Ser 175	Asp
Glu	Asp	Ser	Val 180	Ala	Gly	Ser	Ser	Arg 185	Glu	Ser	Thr	Arg	Lys 190	Gly	Ser
Arg	Ala	Ser 195	Leu	Gly	Ala	Leu	Ser 200	Leu	Glu	Ala	Tyr	Leu 205	Thr	Thr	Gly
Glu	Ala 210	Glu	Thr	Arg	Val	Pro 215	Thr	Met	Arg	Pro	Ser 220	Met	Ser	Gly	Leu
His 225	Leu	Val	Lys	Arg	Gly 230	Arg	Glu	His	Lys	Lys 235	Leu	Asp	Leu	His	Arg 240
Asp	Phe	Thr	Val	Ala 245	Ser	Pro	Ala	Glu	Phe 250	Val	Thr	Arg	Phe	Gly 255	Gly
Asp	Arg	Val	Ile 260	Glu	Lys	Val	Leu	Ile 265	Ala	Asn	Asn	Gly	Ile 270	Ala	Ala
Val	Lys	Cys 275	Met	Arg	Ser	Ile	Arg 280	Arg	Trp	Ala	Tyr	Glu 285	Met	Phe	Arg
Asn	Glu 290	Arg	Ala	Ile	Arg	Phe 295	Val	Val	Met	Val	Thr 300	Pro	Glu	Asp	Leu
Lys 305	Ala	Asn	Ala	Glu	Tyr 310	Ile	Lys	Met	Ala	Asp 315	His	Tyr	Val	Pro	Val 320

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1	Asp	Ile	Ala	Lys 340	Arg	Ile	Pro	Leu	Gln 345	Ala	Val	Trp	Ala	Gly 350	Trp	Gly
1	His	Ala	Ser 355	Glu	Asn	Pro	Lys	Leu 360	Pro	Glu	Leu	Leu	Cys 365	Lys	Asn	Gly
7	Val	Ala 370	Phe	Leu	Gly	Pro	Pro 375	Ser	Glu	Ala	Met	Trp 380	Ala	Leu	Gly	Asp
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	Gln	Gln	Gly	Lys 420	Arg	Ile	Ser	Val	Pro 425	Glu	Asp	Val	Tyr	Asp 430	Lys	Gly
	Cys	Val	Lys 435	Asp	Val	Asp	Glu	Gly 440	Leu	Glu	Ala	Ala	Glu 445	Arg	Ile	Gly
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	Lys	Ile 530		Glu	Glu	Ala	Pro 535		Thr	Ile	Ala	Pro 540	Leu	Ala	Ile	Phe
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Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser I 565 570 575	Phe
His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys 5	Гhr
Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile A 595 600 605	Ala
Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr ( 610 615 620	Зlу
Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser A	Asn 640
Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser 655 655	3lu
Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu I 660 665 670	Leu
Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala A 675 680 685	Ala
Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys I 690 695 700	Phe
Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val 705 710 715	Ala 720
Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu 7735 730 735	-
Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile A	4sp
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tgc atg cgg tct atc cgt agg tgg tct tat gaa atg ttt cga aat gaa Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu 35 40 45	144												
cgt gca att aga ttc gtt gtc atg gtc aca cct gaa gac ctt aaa gcc Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala 50 55 60	192												
aat gca gaa tac att aag atg gca gat cac tat gtg cca gtg cct gga Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly 65 70 75 80	240												
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tct gag aat ccc aaa cta ccg gaa ctt ctc ttg aaa aat ggc att gcc Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala 115 120 125	384												
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gtt Val	cct Pro	gga Gly	tct Ser	ccc Pro 245	ata Ile	ttt Phe	gtg Val	atg Met	aga Arg 250	cta Leu	gcc Ala	aaa Lys	caa Gln	tct Ser 255	cgt Arg	768
cat His	ctg Leu	gag Glu	gtg Val 260	cag Gln	atc Ile	tta Leu	gcg Ala	gac Asp 265	caa Gln	tat Tyr	ggc Gly	aat Asn	gct Ala 270	atc Ile	tct Ser	816
ttg Leu	ttt Phe	ggt Gly 275	cgt Arg	gat Asp	tgc Cys	tct Ser	gta Val 280	caa Gln	cgc Arg	agg Arg	cat His	cag Gln 285	aag Lys	att Ile	att Ile	864
gaa Glu	gaa Glu 290	gca Ala	cct Pro	gct Ala	act Thr	att Ile 295	gct Ala	act Thr	cca Pro	gca Ala	gta Val 300	ttt Phe	gaa Glu	cac His	atg Met	912
					aaa Lys 310											960
					ctg Leu											1008
gaa Glu	ttg Leu	aat Asn	cct Pro 340	cgg Arg	ctg Leu	cag Gln	gta Val	gag Glu 345	cac His	cct Pro	tgt Cys	aca Thr	gag Glu 350	atg Met	gtg Val	1056
gct Ala	gat Asp	gtc Val 355	aat Asn	ctc Leu	cct Pro	gca Ala	gca Ala 360	cag Gln	ctc Leu	cag Gln	att Ile	gcc Ala 365	atg Met	Gly aaa	att Ile	1104
					aag Lys											1152
					att Ile 390											1200
cca Pro	agg Arg	ggc	cat His	gtt Val 405	att Ile	gct Ala	gct Ala	cgg Arg	atc Ile 410	act Thr	agt Ser	gaa Glu	aat Asn	cca Pro 415	gat Asp	1248
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		Glu			gat Asp											1392

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Cys Met Arg 35	Ser Ile	Arg Arg	Trp Ser	Tyr G	Glu Met	Phe Arg 45	Asn	Glu	
Arg Ala Ile	Arg Phe	Val Val 55	Met Val	Thr P	Pro Glu 60	Asp Leu	Lys	Ala	
Asn Ala Glu 65	Tyr Ile	Lys Met 70	Ala Asp		Tyr Val 75	Pro Val	Pro	Gly 80	
Gly Pro Asn	Asn Asn 85	Asn Tyr	Ala Asn	Val G 90	Glu Leu	Ile Leu	Asp 95	Ile	
Ala Lys Arg	Ile Pro 100	Val Gln	Ala Val 105		Ala Gly	Trp Gly		Ala	
Ser Glu Asn 115		Leu Pro	Glu Leu 120	ı Leu L	Leu Lys	Asn Gly 125	Ile	Ala	

Phe	Met 130	Gly	Pro	Pro	Ser	Gln 135	Ala	Met	Trp	Ala	Leu 140	Gly	Asp	Lys	Ile
Ala 145	Ser	Ser	Ile	Val	Ala 150	Gln	Thr	Ala	Gly	Ile 155	Pro	Thr	Leu	Pro	Trp 160
Ser	Gly	Ser	Gly	Leu 165	Arg	Val	Asp	Trp	Gln 170	Glu	Asn	Asp	Phe	Ser 175	Lys
Arg	Ile	Leu	Asn 180	Val	Pro	Gln	Glu	Leu 185	Tyr	Glu	Lys	Gly	Tyr 190	Val	Lys
Asp	Val	Asp 195	Asp	Gly	Leu	Lys	Ala 200	Ala	Glu	Glu	Val	Gly 205	Tyr	Pro	Val
Met	Ile 210	Lys	Ala	Ser	Glu	Gly 215	Gly	Gly	Gly	Lys	Gly 220	Ile	Arg	Lys	Val
Asn 225	Asn	Ala	Asp	Asp	Phe 230	Pro	Asn	Leu	Phe	Arg 235	Gln	Val	Gln	Ala	Glu 240
Val	Pro	Gly	Ser	Pro 245	Ile	Phe	Val	Met	Arg 250	Leu	Ala	Lys	Gln	Ser 255	Arg
His	Leu	Glu	Val 260	Gln	Ile	Leu	Ala	Asp 265	Gln	Tyr	Gly	Asn	Ala 270	Ile	Ser
Leu	Phe	Gly 275	Arg	Asp	Cys	Ser	Val 280	Gln	Arg	Arg	His	Gln 285	Lys	Ile	Ile
Glu	Glu 290	Ala	Pro	Ala	Thr	Ile 295	Ala	Thr	Pro	Ala	Val 300	Phe	Glu	His	Met
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Gly	Thr	Val	Glu	Tyr 325	Leu	Tyr	Ser	Gln	Asp 330	Gly	Ser	Phe	Tyr	Phe 335	Leu
Glu	Leu	Asn	Pro 340	Arg	Leu	Gln	Val	Glu 345	His	Pro	Cys	Thr	Glu 350	Met	Val
Ala	Asp	Val 355	Asn	Leu	Pro	Ala	Ala 360	Gln	Leu	Gln	Ile	Ala 365	Met	Gly	Ile
Pro	Leu	Tyr	Arg	Ile	Lys	Asp	Ile	Arg	Met	Met	Tyr	Gly	Val	Ser	Pro

Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala His Val Pro Cys 385 390 400

Pro Arg Gly	His Val 405	Ile Ala	Ala Arg	Ile Thr 410	Ser Glu		ro Asp 15
Glu Gly Phe	Lys Pro 420	Ser Ser	Gly Thr 425	Val Gln	Glu Leu	Asn Pi	he Arg
Ser Asn Lys 435		Trp Gly	Tyr Phe	Ser Val	Ala Ala 445	Ala G	ly Gly
Leu His Glu 450	Phe Ala	Asp Ser 455	Gln Phe	Gly His	Cys Phe 460	Ser T	rp Gly
Glu Asn Arg 465		Ala Ile 470	Ser Asn	Met Val 475	Val Ala	Leu L	ys Glu 480
Leu Ser Ile	Arg Gly 485	Asp Phe	Arg Thr	Thr Val 490	Glu Tyr		le Lys 95
Leu Leu Glu	Thr Glu 500	Ser Phe	Gln Met 505		Ile Asp	Thr G 510	ly Trp
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gtc atc gag Val Ile Glu							

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Cys	Met	Arg 35	Ser	Ile	Arg	Arg	Trp 40	Ala	Tyr	Glu	Met	Phe 45	Arg	Asn	Glu	
	_				_	gtg Val 55	_	-				_			_	192
	_				_	atg Met		_			_		_			240
						tat Tyr	_				_			_		288
						cag Gln										336
						ccg Pro		_	_	_	_			_		384
						gag Glu 135								_		432
						cag Gln	-		_	-			_			480
						gtg Val										528
						cca Pro										576
	_	_	_			ttg Leu		_	_	_	_					624
						gaa Glu 215										672
						ttc Phe								_	-	720
						atc Ile										768
						atc Ile										816

										cgg Arg					864
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_							-	-		ggc Gly					1008
_		_		_	_	_		_		ccc Pro	_		_	_	1056
	_	_	_	_	_	-	_	_		cag Gln			_		1104
										ctg Leu 380					1152
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	-	_	_					_	_	gtg Val		_	_	_	1344
	_			-	-					cac His 460					1392
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										gac Asp					1536

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Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala 50 55 60	
Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly 65 70 75 80	
Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile 85 90 95	
Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110	
Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala 115 120 125	
Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile 130 135 140	
Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg 145 150 155 160	
Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln 165 170 175	

Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val

180 185 190

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Ala 225	Glu	Ser	Ala	Glu	Asp 230	Phe	Pro	Ile	Leu	Phe 235	Arg	Gln	Val	Gln	Ser 240
Glu	Ile	Pro	Gly	Ser 245	Pro	Ile	Phe	Leu	Met 250	Lys	Leu	Ala	Gln	His 255	Ala
Arg	His	Leu	Glu 260	Val	Gln	Ile	Leu	Ala 265	Asp	Gln	Tyr	Gly	Asn 270	Ala	Val
Ser	Leu	Phe 275	Gly	Arg	Asp	Cys	Ser 280	Ile	Gln	Arg	Arg	His 285	Gln	Lys	Ile
Val	Glu 290	Glu	Ala	Pro	Ala	Thr 295	Ile	Ala	Pro	Leu	Ala 300	Ile	Phe	Glu	Phe
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Ala	Gly	Thr	Val	Glu 325	Tyr	Leu	Tyr	Ser	Gln 330	Asp	Gly	Ser	Phe	His 335	Phe
Leu	Glu	Leu	Asn 340	Pro	Arg	Leu	Gln	Val 345	Glu	His	Pro	Cys	Thr 350	Glu	Met
Ile	Ala	Asp 355	Val	Asn	Leu	Pro	Ala 360	Ala	Gln	Leu	Gln	Ile 365	Ala	Met	Gly
Val	Pro 370	Leu	His	Arg	Leu	Lys 375	Asp	Ile	Arg	Leu	Leu 380	Tyr	Gly	Glu	Ser
Pro 385	Trp	Gly	Val	Thr	Pro 390	Ile	Ser	Phe	Glu	Thr 395	Pro	Ser	Asn	Pro	Pro 400
Leu	Ala	Arg	Gly	His 405	Val	Ile	Ala	Ala	Arg 410	Ile	Thr	Ser	Glu	Asn 415	Pro
Asp	Glu	Gly	Phe 420	Lys	Pro	Ser	Ser	Gly 425	Thr	Val	Gln	Glu	Leu 430	Asn	Phe

Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly
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440
445

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Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys 465 470 475 480

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Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly 500 505 510

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<221> MISC\_FEATURE

<222> (1)..(554)

<223> N-terminal deleted Ustilago ACCase BC domain (AAs 7-560)

<400> 17

Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro 1 5 10 15

Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val 20 25 30

Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu 35 40 45

Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg 50 55 60

Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn 65 70 75 80

1	Ala	Asp	Tyr	IIe	Arg 85	Met	АІА	Asp	GIN	90	Val	GIU	vai	PIO	95 95	GIY
	Ser	Asn	Asn	Asn 100	Asn	Tyr	Ala	Asn	Val 105	Asp	Leu	Ile	Val	Asp 110	Val	Ala
•	Glu	Arg	Ala 115	Gly	Val	His	Ala	Val 120	Trp	Ala	Gly	Trp	Gly 125	His	Ala	Ser
,	Glu	Asn 130	Pro	Arg	Leu	Pro	Glu 135	Ser	Leu	Ala	Ala	Ser 140	Lys	His	Lys	Ile
	Ile 145	Phe	Ile	Gly	Pro	Pro 150	Gly	Ser	Ala	Met	Arg 155	Ser	Leu	Gly	Asp	Lys 160
	Ile	Ser	Ser	Thr	Ile 165	Val	Ala	Gln	His	Ala 170	Asp	Val	Pro	Cys	Met 175	Pro
	Trp	Ser	Gly	Thr 180	Gly	Ile	Lys	Glu	Thr 185	Met	Met	Ser	Asp	Gln 190	Gly	Phe
	Leu	Thr	Val 195	Ser	Asp	Asp	Val	Tyr 200	Gln	Gln	Ala	Cys	Ile 205	His	Thr	Ala
	Glu	Glu 210	Gly	Leu	Glu	Lys	Ala 215	Glu	Lys	Ile	Gly	Tyr 220	Pro	Val	Met	Ile
	Lys 225	Ala	Ser	Glu	Gly	Gly 230	Gly	Gly	Lys	Gly	Ile 235	Arg	Lys	Cys	Thr	Asn 240
	Gly	Glu	Glu	Phe	Lys 245	Gln	Leu	Tyr	Asn	Ala 250	Val	Leu	Gly	Glu	Val 255	Pro
	Gly	Ser	Pro	Val 260	Phe	Val	Met	Lys	Leu 265	Ala	Gly	Gln	Ala	Arg 270	His	Leu
	Glu	Val	Gln 275	Leu	Leu	Ala	Asp	Gln 280	Tyr	Gly	Asn	Ala	Ile 285	Ser	Ile	Phe
	Gly	Arg 290		Cys	Ser	Val	Gln 295	Arg	Arg	His	Gln	Lys 300	Ile	Ile	Glu	Glu
	Ala 305	Pro	Val	Thr	Ile	Ala 310	Pro	Glu	Asp	Ala	Arg 315	Glu	Ser	Met	Glu	Lys 320

- Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr 325 330 335
- Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu 340 345 350
- Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser 355 360 365
- Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro 370 375 380
- Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg 385 390 395 400
- Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys 405 410 415
- Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile 420 425 430
- Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu 435 440 445
- Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser 450 455 460
- Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly
  465 470 475 480
- His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met 485 490 495
- Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr 500 505 510
- Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn 515 520 525
- Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr 530 540
- Ala Glu Arg Pro Pro Ala Asp Leu Ala Val 545 550

- <210> 18
- <211> 549
- <212> PRT
- <213> Ustilago maydis
- <220>

- <221> MISC\_FEATURE <222> (1)..(549) <223> N-terminal deleted Ustilago ACCase BC domain (AAs 12-560)
- <400> 18
- Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala 5 10
- Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu 20 25
- Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg 40
- Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr 50
- Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg 70 75
- Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn 85 90
- Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val 100 105
- His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu 120
- Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro 130 135
- Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile 150
- Val Ala Gln His Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly 170
- Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp 185 190

Asp Val Tyr 195	Gln Gln	Ala Cys	Ile Hi 200	s Thr A	Ala Glu	Glu Gly 205	/ Leu	Glu
Lys Ala Glu 210	Lys Ile	Gly Tyr 215		al Met :	Ile Lys 220	Ala Ser	Glu	Gly
Gly Gly Gly 225	Lys Gly	Ile Arg 230	Lys Cy		Asn Gly 235	Glu Glı	ı Phe	Lys 240
Gln Leu Tyr	Asn Ala 245	Val Leu	Gly Gl	u Val 1 250	Pro Gly	Ser Pro	Val 255	Phe
Val Met Lys	Leu Ala 260	Gly Gln	Ala Ar 26	_	Leu Glu	Val Glr 270		Leu
Ala Asp Gln 275		Asn Ala	Ile Se 280	er Ile 1	Phe Gly	Arg Ası 285	Cys	Ser
Val Gln Arg 290	Arg His	Gln Lys 295		e Glu (	Glu Ala 300	Pro Val	. Thr	Ile
Ala Pro Glu 305	Asp Ala	Arg Glu 310	Ser Me		Lys Ala 315	Ala Val	. Arg	Leu 320
Ala Lys Leu	Val Gly 325	Tyr Val	Ser Al	a Gly :	Thr Val	Glu Tr	335	Tyr
Ser Pro Glu	Ser Gly 340	Glu Phe	Ala Ph 34		Glu Leu	Asn Pro		Leu
Gln Val Glu 355			Glu Me 360	et Val S	Ser Gly	Val Asr 365	ı Ile	Pro
Ala Ala Gln 370	Leu Gln	Val Ala 375		y Ile 1	Pro Leu 380	Tyr Sei	: Ile	Arg
Asp Ile Arg 385	Thr Leu	Tyr Gly 390	Met As		Arg Gly 395	Asn Glu	ı Val	Ile 400
Asp Phe Asp	Phe Ser 405	Ser Pro	Glu Se	er Phe 1 410	Lys Thr	Gln Arg	Lys 415	Pro
Gln Pro Gln	Gly His 420	Val Val	Ala Cy 42		Ile Thr	Ala Glu 430		Pro
Asp Thr Gly	Phe Lys	Pro Gly	Met Gl	y Ala I	Leu Thr	Glu Lev	. Asn	Phe

435 440 445

Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly 450 455 460

Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr 465 470 475 480

Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys 485 490 495

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile 500 505 510

Lys Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly 515 520 525

Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro 530 540

Ala Asp Leu Ala Val 545

<210> 19

<211> 539

<212> PRT

<213> Ustilago maydis

<220>

<221> MISC\_FEATURE

<222> (1)..(539)

<223> N-terminal deleted Ustilago ACCse BC domain (AAs 22-560)

<400> 19

Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser 1 10 15

Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys 20 25 30

Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu
35 40 45

Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val 50 60

Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly

Gly Ser Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val 85 90 95

Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110

Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys 115 120 125

Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp 130 135 140

Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met 145 150 155 160

Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly 165 170 175

Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr 180 185 190

Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met 195 200 205

Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr 210 215 220

Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val 225 230 235 240

Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His 245 250 255

Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile 260 265 270

Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu 275 280 285

Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu 290 295 300

Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly 305 310 315 320

Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro Ala Asp Leu Ala Val <210> 20

<211> 529 <212> PRT

- <213> Ustilago maydis
- <220>
- <221> MISC\_FEATURE
- <222> (1)..(529)
- <223> N-terminal deleted Ustilago ACCase BC domain (AAs 32-560)
- <400> 20
- Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn 1 5 10 15
- Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr 20 25 30
- Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr 35 40 45
- Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln 50 55
- Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val 65 70 75 80
- Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp 85 90 95
- Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu 100 105 110
- Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala 115 120 125
- Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His 130 135 140
- Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr 145 150 155 160
- Met Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln
  165 170 175
- Gln Ala Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys 180 185 190
- Ile Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys 195 200 205

Gly Ile Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu

Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg 450 455 Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile 470 475 Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu 485 490 Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly 500 505 Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro Ala Asp Leu Ala 515 520 Val <210> 21 <211> 519 <212> PRT <213> Ustilago maydis <220> <221> MISC\_FEATURE <222> (1)..(519) <223> N-terminal deleted Ustilago ACCase BC domain (AAs 42-560) <400> 21 Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr 35 40 Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn 50 Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala 65 75

90

Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro

Arg Leu Pro	Glu Ser 100	Leu Al	a Ala	Ser 105	Lys	His	Lys	Ile	Ile 110	Phe	Ile
Gly Pro Pro 115	Gly Ser	Ala Me	t Arg 120	Ser	Leu	Gly	Asp	Lys 125	Ile	Ser	Ser
Thr Ile Val	Ala Gln	His Al		Val	Pro	Cys	Met 140	Pro	Trp	Ser	Gly
Thr Gly Ile 145	Lys Glu	Thr Me	t Met	Ser	Asp	Gln 155	Gly	Phe	Leu	Thr	Val 160
Ser Asp Asp	Val Tyr 165	Gln Gl	n Ala	Cys	Ile 170	His	Thr	Ala	Glu	Glu 175	Gly
Leu Glu Lys	Ala Glu 180	Lys Il	e Gly	Tyr 185	Pro	Val	Met	Ile	Lys 190	Ala	Ser
Glu Gly Gly 195	Gly Gly	Lys Gl	y Ile 200	_	Lys	Cys	Thr	Asn 205	Gly	Glu	Glu
Phe Lys Gln 210	Leu Tyr	Asn Al		Leu	Gly	Glu	Val 220	Pro	Gly	Ser	Pro
Val Phe Val 225	Met Lys	Leu Al 230	a Gly	Gln	Ala	Arg 235	His	Leu	Glu	Val	Gln 240
Leu Leu Ala	Asp Gln 245	Tyr Gl	y Asn	Ala	Ile 250	Ser	Ile	Phe	Gly	Arg 255	Asp
Cys Ser Val	Gln Arg 260	-		_					Ala 270	Pro	Val
Thr Ile Ala 275	Pro Glu	Asp Al	a Arg 280	Glu	Ser	Met	Glu	Lys 285	Ala	Ala	Val
Arg Leu Ala 290	Lys Leu	Val Gl		Val	Ser	Ala	Gly 300	Thr	Val	Glu	Trp
Leu Tyr Ser 305	Pro Glu	Ser G] 310	y Glu	Phe	Ala	Phe 315	Leu	Glu	Leu	Asn	Pro 320
Arg Leu Gln	Val Glu 325	His Pr	o Thr	Thr	Glu 330	Met	Val	Ser	Gly	Val 335	Asn
Ile Pro Ala	Ala Gln	Leu Gl	n Val	Ala	Met	Gly	Ile	Pro	Leu	Tyr	Ser

340 345 350

Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu 355 360 365

Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg 370 375 380

Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile Thr Ala Glu 385 390 395 400

Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu 405 410 415

Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr 420 425 430

Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe 435 440 imes 445

Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser 450 455 460

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr 465 470 475 480

Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr 485 490 495

Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg 500 505 510

Pro Pro Ala Asp Leu Ala Val 515

<210> 22

<211> 554

<212> PRT

<213> Ustilago maydis

<220>

<221> MISC\_FEATURE

<222> (1)..(554)

<223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-555)

<400> 22

Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro

Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln 

Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile 

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr 

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val

Glu Val Pro Gly Gly Ser Asn Asn Asn Tyr Ala Asn Val Asp Leu 

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly 

Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala 

Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg 

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp 

Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met 

Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala 

Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly 

Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile 

Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val 

Leu	Gly	Glu	Val 260	Pro	Gly	Ser	Pro	Val 265	Phe	Val	Met	Lys	Leu 270	Ala	Gly
Gln	Ala	Arg 275	His	Leu	Glu	Val	Gln 280	Leu	Leu	Ala	Asp	Gln 285	Tyr	Gly	Asn
Ala	Ile 290	Ser	Ile	Phe	Gly	Arg 295	Asp	Cys	Ser	Val	Gln 300	Arg	Arg	His	Gln
Lys 305	Ile	Ile	Glu	Glu	Ala 310	Pro	Val	Thr	Ile	Ala 315	Pro	Glu	Asp	Ala	Arg 320
Glu	Ser	Met	Glu	Lys 325	Ala	Ala	Val	Arg	Leu 330	Ala	Lys	Leu	Val	Gly 335	Tyr
Val	Ser	Ala	Gly 340	Thr	Val	Glu	Trp	Leu 345	Tyr	Ser	Pro	Glu	Ser 350	Gly	Glu
Phe	Ala	Phe 355	Leu	Glu	Leu	Asn	Pro 360	Arg	Leu	Gln	Val	Glu 365	His	Pro	Thr
Thr	Glu 370	Met	Val	Ser	Gly	Val 375	Asn	Ile	Pro	Ala	Ala 380	Gln	Leu	Gln	Val
Ala 385	Met	Gly	Ile	Pro	Leu 390	Tyr	Ser	Ile	Arg	Asp 395	Ile	Arg	Thr	Leu	Tyr 400
Gly	Met	Asp	Pro	Arg 405	Gly	Asn	Glu	Val	Ile 410		Phe	Asp	Phe	Ser 415	Ser
Pro	Glu	Ser	Phe 420	Lys	Thr	Gln	Arg	Lys 425	Pro	Gln	Pro	Gln	Gly 430	His	Val
Val	Ala	Cys 435		Ile	Thr	Ala	Glu 440		Pro	Asp	Thr	Gly 445		Lys	Pro
Gly	Met 450	_	Ala	Leu	Thr	Glu 455		Asn	Phe	Arg	Ser 460		Thr	Ser	Thr
Trp 465	_	Tyr	Phe	Ser	Val 470	Gly	Thr	Ser	Gly	Ala 475		His	Glu	Tyr	Ala 480
Asp	Ser	Gln	Phe	Gly 485	His	Ile	Phe	Ala	Tyr 490		Ala	Asp	Arg	Ser 495	Glu

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Glu Thr Asp 520 515 Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro 550 <210> 23 <211> 549 <212> PRT <213> Ustilago maydis <220> <221> MISC FEATURE <222> (1)..(549) <223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-550) <400> 23 Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile 35 40 Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr 50 Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu 70 75 65 Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val 85 90

58

110

125

Glu Val Pro Gly Gly Ser Asn Asn Asn Tyr Ala Asn Val Asp Leu

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly

120

105

100

Trp	Gly 130	His	Ala	Ser	Glu	Asn 135	Pro	Arg	Leu	Pro	Glu 140	Ser	Leu	Ala	Ala
Ser 145	Lys	His	Lys	Ile	Ile 150	Phe	Ile	Gly	Pro	Pro 155	Gly	Ser	Ala	Met	Arg 160
Ser	Leu	Gly	Asp	Lys 165	Ile	Ser	Ser	Thr	Ile 170	Val	Ala	Gln	His	Ala 175	Asp
Val	Pro	Cys	Met 180	Pro	Trp	Ser	Gly	Thr 185	Gly	Ile	Lys	Glu	Thr 190	Met	Met
Ser	Asp	Gln 195	Gly	Phe	Leu	Thr	Val 200	Ser	Asp	Asp	Val	Tyr 205	Gln	Gln	Ala
Cys	Ile 210	His	Thr	Ala	Glu	Glu 215	Gly	Leu	Glu	Lys	Ala 220	Glu	Lys	Ile	Gly
Tyr 225	Pro	Val	Met	Ile	Lys 230	Ala	Ser	Glu	Gly	Gly 235	Gly	Gly	Lys	Gly	Ile 240
Arg	Lys	Cys	Thr	Asn 245	Gly	Glu	Glu	Phe	Lys 250	Gln	Leu	Tyr	Asn	Ala 255	Val
Leu	Gly	Glu	Val 260	Pro	Gly	Ser	Pro	Val 265	Phe	Val	Met	Lys	Leu 270	Ala	Gly
Gln	Ala	Arg 275	His	Leu	Glu	Val	Gln 280	Leu	Leu	Ala	Asp	Gln 285	Tyr	Gly	Asn
Ala	Ile 290	Ser	Ile	Phe	Gly	Arg 295	Asp	Cys	Ser	Val	Gln 300	Arg	Arg	His	Gln
Lys 305	Ile	Ile	Glu	Glu	Ala 310	Pro	Val	Thr	Ile	Ala 315	Pro	Glu	Asp	Ala	Arg 320
Glu	Ser	Met	Glu	Lys 325		Ala	Val	Arg	Leu 330	Ala	Lys	Leu	Val	Gly 335	Tyr
Val	Ser	Ala	Gly 340	Thr	Val	Glu	Trp	Leu 345	Tyr	Ser	Pro	Glu	Ser 350	Gly	Glu
Phe	Ala	Phe 355		Glu	Leu	Asn	Pro 360	Arg	Leu	Gln	Val	Glu 365	His	Pro	Thr

Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val 375 Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr 395 Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser 410 405 Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val 425 420 Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro 440 435 Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr 455 450 Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala 475 470 465 Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu 490 485 Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly 505 500 Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp 515 520 Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile 535 530 Gln Asp Arg Leu Thr 545 <210> 24 <211> 539 <212> PRT <213> Ustilago maydis <220> <221> MISC\_FEATURE <222> (1)..(539) <223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-540)

<400> 24

Pro 1	Pro	Pro	Asp	His 5	Lys	Ala	Val	Ser	Gln 10	Phe	Ile	Gly	Gly	Asn 15	Pro
Leu	Glu	Thr	Ala 20	Pro	Ala	Ser	Pro	Val 25	Ala	Asp	Phe	Ile	Arg 30	Lys	Gln
Gly	Gly	His 35	Ser	Val	Ile	Thr	Lys 40	Val	Leu	Ile	Cys	Asn 45	Asn	Gly	Ile
Ala	Ala 50	Val	Lys	Glu	Ile	Arg 55	Ser	Ile	Arg	Lys	Trp 60	Ala	Tyr	Glu	Thr
Phe 65	Gly	Asp	Glu	Arg	Ala 70	Ile	Glu	Phe	Thr	Val 75	Met	Ala	Thr	Pro	Glu 80
Asp	Leu	Lys	Val	Asn 85	Ala	Asp	Tyr	Ile	Arg 90	Met	Ala	Asp	Gln	Tyr 95	Val
Glu	Val	Pro	Gly 100	Gly	Ser	Asn	Asn	Asn 105	Asn	Tyr	Ala	Asn	Val 110	Asp	Leu
Ile	Val	Asp 115	Val	Ala	Glu	Arg	Ala 120	Gly	Val	His	Ala	Val 125	Trp	Ala	Gly
Trp	Gly 130	His	Ala	Ser	Glu	Asn 135	Pro	Arg	Leu	Pro	Glu 140	Ser	Leu	Ala	Ala
Ser 145	Lys	His	Lys	Ile	Ile 150	Phe	Ile	Gly	Pro	Pro 155	Gly	Ser	Ala	Met	Arg 160
Ser	Leu	Gly	Asp	Lys 165	Ile	Ser	Ser	Thr	Ile 170	Val	Ala	Gln	His	Ala 175	Asp
Val	Pro	Cys	Met 180	Pro	Trp	Ser	Gly	Thr 185	Gly	Ile	Lys	Glu	Thr 190	Met	Met
Ser	Asp	Gln 195	Gly	Phe	Leu	Thr	Val 200	Ser	Asp	Asp	Val	Tyr 205	Gln	Gln	Ala
Cys	Ile 210	His	Thr	Ala	Glu	Glu 215	Gly	Leu	Glu	Lys	Ala 220	Glu	Lys	Ile	Gly
Tyr 225	Pro	Val	Met	Ile	Lys 230	Ala	Ser	Glu	Gly	Gly 235	Gly	Gly	Lys	Gly	Ile 240
Arg	Lys	Cys	Thr	Asn	Gly	Glu	Glu	Phe	Lys	Gln	Leu	Tyr	Asn	Ala	Val

- Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly 260 265 270
- Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn 275 280 285
- Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln 290 295 300
- Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg 305 310 315 320
- Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr 325 330 335
- Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu 340 345 350
- Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr 355 360 365
- Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val 370 380
- Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr 385 390 395 400
- Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser 405 410 415
- Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val 420 425 430
- Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro 435 440 445
- Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr 450 455 460
- Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala 465 470 475 480
- Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu 485 490 495

- Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly 500 505
- Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp 515 520
- Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp 530 535
- <210> 25
- <211> 529 <212> PRT
- <213> Ustilago maydis
- <220>
- <221> MISC\_FEATURE
- <222> (1)..(529)
- <223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-530)
- Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro 5 10
- Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln 25
- Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile 40
- Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr 55
- Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu 70 75
- Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val 90
- Glu Val Pro Gly Gly Ser Asn Asn Asn Tyr Ala Asn Val Asp Leu 100
- Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly 115 . 120
- Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala 130 135 140

Ser Lys His 145	Lys Ile	Ile Phe 150	Ile G	Gly Pro	Pro Gly 155	Ser	Ala	Met	Arg 160
Ser Leu Gly	Asp Lys 165	Ile Ser	Ser I	Thr Ile 170	Val Ala	Gln	His	Ala 175	Asp
Val Pro Cys	Met Pro 180	Trp Ser		Thr Gly 185	Ile Lys	Glu	Thr 190	Met	Met
Ser Asp Gln 195	Gly Phe	Leu Thr	Val S 200	Ser Asp	Asp Val	Tyr 205	Gln	Gln	Ala
Cys Ile His 210	Thr Ala	Glu Glu 215	_	Leu Glu	Lys Ala 220	Glu	Lys	Ile	Gly
Tyr Pro Val 225	Met Ile	Lys Ala 230	Ser G	Glu Gly	Gly Gly 235	Gly	Lys	Gly	Ile 240
Arg Lys Cys	Thr Asn 245	Gly Glu	. Glu F	Phe Lys 250	Gln Leu	Tyr	Asn	Ala 255	Val
Leu Gly Glu	Val Pro 260	Gly Ser		Val Phe 265	Val Met	Lys	Leu 270	Ala	Gly
Gln Ala Arg 275	His Leu	Glu Val	Gln I 280	Leu Leu	Ala Asp	Gln 285	Tyr	Gly	Asn
Ala Ile Ser 290	Ile Phe	Gly Arg 295		Cys Ser	Val Gln 300	Arg	Arg	His	Gln
Lys Ile Ile 305		Ala Pro	Val T		Ala Pro 315	Glu	Asp		Arg 320
Glu Ser Met	Glu Lys 325	Ala Ala	. Val A	Arg Leu 330	Ala Lys	Leu	Val	Gly 335	Tyr
Val Ser Ala	Gly Thr 340	Val Glu	_	Leu Tyr 345	Ser Pro		Ser 350	Gly	Glu
Phe Ala Phe 355	Leu Glu	Leu Asn	Pro A	Arg Leu	Gln Val	Glu 365	His	Pro	Thr
Thr Glu Met 370	Val Ser	Gly Val		Ile Pro	Ala Ala	Gln	Leu	Gln	Val

Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr 390 395 Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser 405 Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val 425 Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro 440 Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr 455 460 Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala 470 475 Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu 485 490 Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly 500 505 Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp 515 520 Ala <210> 26 <211> 519 <212> PRT

<213> Ustilago maydis

<220>

<221> MISC\_FEATURE

<222> (1)..(519)

<223> C-terminal deleted Ustilago ACCase BC domain (AAs2-520)

<400> 26

Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro 5 15

Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln 20 30

Gly	Gly	His 35	Ser	Val	Ile	Thr	Lys 40	Val	Leu	Ile	Cys	Asn 45	Asn	Gly	Ile
Ala	Ala 50	Val	Lys	Glu	Ile	Arg 55	Ser	Ile	Arg	Lys	Trp 60	Ala	Tyr	Glu	Thr
Phe 65	Gly	Asp	Glu	Arg	Ala 70	Ile	Glu	Phe	Thr	Val 75	Met	Ala	Thr	Pro	Glu 80
Asp	Leu	Lys	Val	Asn 85	Ala	Asp	Tyr	Ile	Arg 90	Met	Ala	Asp	Gln	Tyr 95	Val
Glu	Val	Pro	Gly 100	Gly	Ser	Asn	Asn	Asn 105	Asn	Tyr	Ala	Asn	Val 110	Asp	Leu
Ile	Val	Asp 115	Val	Ala	Glu	Arg	Ala 120	Gly	Val	His	Ala	Val 125	Trp	Ala	Gly
Trp	Gly 130	His	Ala	Ser	Glu	Asn 135	Pro	Arg	Leu	Pro	Glu 140	Ser	Leu	Ala	Ala
Ser 145	Lys	His	Lys	Ile	Ile 150	Phe	Ile	Gly	Pro	Pro 155	Gly	Ser	Ala	Met	Arg 160
Ser	Leu	Gly	Asp	Lys 165	Ile	Ser	Ser	Thr	Ile 170	Val	Ala	Gln	His	Ala 175	Asp
Val	Pro	Cys	Met 180	Pro	Trp	Ser	Gly	Thr 185	Gly	Ile	Lys	Glu	Thr 190	Met	Met
Ser	Asp	Gln 195	Gly	Phe	Leu	Thr	Val 200	Ser	Asp	Asp	Val	Tyr 205	Gln	Gln	Ala
Cys	Ile 210	His	Thr	Ala	Glu	Glu 215	Gly	Leu	Glu	Lys	Ala 220	Glu	Lys	Ile	Gly
Tyr 225	Pro	Val	Met	Ile	Lys 230	Ala	Ser	Glu	Gly	Gly 235	Gly	Gly	Lys	Gly	Ile 240
Arg	Lys	Cys	Thr	Asn 245	Gly	Glu	Glu	Phe	Lys 250	Gln	Leu	Tyr	Asn	Ala 255	Val
Leu	Gly	Glu	Val 260	Pro	Gly	Ser	Pro	Val 265	Phe	Val	Met	Lys	Leu 270	Ala	Gly

Gln Ala Arg 275	His Leu	Glu Val	280	Leu	Leu	Ala	Asp	Gln 285	Tyr	Gly	Asn
Ala Ile Ser 290	Ile Phe	Gly Arg	_	Cys	Ser	Val	Gln 300	Arg	Arg	His	Gln
Lys Ile Ile 305	Glu Glu	Ala Pro 310	Val	Thr	Ile	Ala 315	Pro	Glu	Asp	Ala	Arg 320
Glu Ser Met	Glu Lys 325	Ala Ala	a Val	Arg	Leu 330	Ala	Lys	Leu	Val	Gly 335	Tyr
Val Ser Ala	Gly Thr 340	Val Glu	ı Trp	Leu 345	Tyr	Ser	Pro	Glu	Ser 350	Gly	Glu
Phe Ala Phe 355	Leu Glu	Leu Ası	1 Pro 360	Arg	Leu	Gln	Val	Glu 365	His	Pro	Thr
Thr Glu Met 370	Val Ser	Gly Val		Ile	Pro	Ala	Ala 380	Gln	Leu	Gln	Val
Ala Met Gly 385	Ile Pro	Leu Tyı 390	Ser	Ile	Arg	Asp 395	Ile	Arg	Thr	Leu	Tyr 400
Gly Met Asp	Pro Arg 405	Gly Asr	ı Glu	Val	Ile 410	Asp	Phe	Asp	Phe	Ser 415	Ser
Pro Glu Ser	Phe Lys 420	Thr Glr	n Arg	Lys 425	Pro	Gln	Pro	Gln	Gly 430	His	Val
Val Ala Cys 435	Arg Ile	Thr Ala	Glu 440	Asn	Pro	Asp	Thr	Gly 445	Phe	Lys	Pro
Gly Met Gly 450	Ala Leu	Thr Glu 455		Asn	Phe	Arg	Ser 460	Ser	Thr	Ser	Thr
Trp Gly Tyr 465	Phe Ser	Val Gly 470	Thr	Ser	Gly	Ala 475	Leu	His	Glu	Tyr	Ala 480
Asp Ser Gln	Phe Gly 485	His Ile	. Phe	Ala	Tyr 490	Gly	Ala	Asp	Arg	Ser 495	Glu
Ala Arg Lys	Gln Met 500	Val Ile	e Ser	Leu 505	Lys	Glu	Leu	Ser	Ile 510	Arg	Gly
Asp Phe Arg	Thr Thr	Val Glu	ı								

- <210> 27
- <211> 554
- <212> PRT
- <213> Ustilago maydis
- <220>
- <221> MISC FEATURE
- <222> (1)..(554)
- <223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 4-547)
- <400> 27
- Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu
  1 5 10 15
- Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly
  20 25 30
- His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala 35 40 45
- Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly 50 60
- Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu 65 70 75 80
- Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val 85 90 95
- Pro Gly Gly Ser Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val
  100 105 110
- Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly
  115 120 125
- His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys 130 135 140
- Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro 165 170 175
- Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp

180	185	190

- Gln Gly Phe Leu Thr Val Ser Asp Val Tyr Gln Gln Ala Cys Ile 195 200 205
- His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro 210 215 220
- Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys 225 230 235 240
- Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly
  245 250 255
- Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala
  260 265 270
- Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile 275 280 285
- Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile 290 295 300
- Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser 305 310 315 320
- Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser 325 330 335
- Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala 340 345 350
- Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu 355 360 365
- Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met 370 380
- Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met 385 390 395 400
- Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu 405 410 415
- Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala 420 425 430

Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met 435 440 Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly 455 460 450 Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser 465 470 480 475 Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg 485 490 Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe 500 505 510 Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe 515 520 525 Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp 530 535 540 Arg Leu Thr Ala Glu Arg Pro Pro Ala Asp 545 550 <210> 28 <211> 549 <212> PRT <213> Ustilago maydis <220> <221> MISC\_FEATURE (1)..(549) <223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 7-555) <400> 28 Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val 20 Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu

60

Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg

55

Ala 65	Ile	Glu	Phe	Thr	Val 70	Met	Ala	Thr	Pro	Glu 75	Asp	Leu	Lys	Val	Asn 80
Ala	Asp	Tyr	Ile	Arg 85	Met	Ala	Asp	Gln	Tyr 90	Val	Glu	Val	Pro	Gly 95	Gly
Ser	Asn	Asn	Asn 100	Asn	Tyr	Ala	Asn	Val 105	Asp	Leu	Ile	Val	Asp 110	Val	Ala
Glu	Arg	Ala 115	Gly	Val	His	Ala	Val 120	Trp	Ala	Gly	Trp	Gly 125	His	Ala	Ser
Glu	Asn 130	Pro	Arg	Leu	Pro	Glu 135	Ser	Leu	Ala	Ala	Ser 140	Lys	His	Lys	Ile
Ile 145	Phe	Ile	Gly	Pro	Pro 150	Gly	Ser	Ala	Met	Arg 155	Ser	Leu	Gly	Asp	Lys 160
Ile	Ser	Ser	Thr	Ile 165	Val	Ala	Gln	His	Ala 170	Asp	Val	Pro	Cys	Met 175	Pro
Trp	Ser	Gly	Thr 180	Gly	Ile	Lys	Glu	Thr 185	Met	Met	Ser	Asp	Gln 190	Gly	Phe
Leu	Thr	Val 195	Ser	Asp	Asp	Val	Tyr 200	Gln	Gln	Ala	Cys	Ile 205	His	Thr	Ala
Glu	Glu 210	Gly	Leu	Glu	Lys	Ala 215	Glu	Lys	Ile	Gly	Tyr 220	Pro	Val	Met	Ile
Lys 225	Ala	Ser	Glu	Gly	Gly 230	Gly	Gly	Lys	Gly	Ile 235	Arg	Lys	Cys	Thr	Asn 240
Gly	Glu	Glu	Phe	Lys 245	Gln	Leu	Tyr	Asn	Ala 250	Val	Leu	Gly	Glu	Val 255	Pro
Gly	Ser	Pro	Val 260	Phe	Val	Met	Lys	Leu 265	Ala	Gly	Gln	Ala	Arg 270	His	Leu
Glu	Val	Gln 275	Leu	Leu	Ala	Asp	Gln 280	Tyr	Gly	Asn	Ala	Ile 285	Ser	Ile	Phe
Gly	Arg 290	Asp	Cys	Ser	Val	Gln 295	Arg	Arg	His	Gln	Lys 300	Ile	Ile	Glu	Glu

Ala 305	Pro	Val	Thr	Ile	Ala 310	Pro	Glu	Asp	Ala	Arg 315	Glu	Ser	Met	Glu	Lys 320
Ala	Ala	Val	Arg	Leu 325	Ala	Lys	Leu	Val	Gly 330	Tyr	Val	Ser	Ala	Gly 335	Thr
Val	Glu	Trp	Leu 340	Tyr	Ser	Pro	Glu	Ser 345	Gly	Glu	Phe	Ala	Phe 350	Leu	Glu
Leu	Asn	Pro 355	Arg	Leu	Gln	Val	Glu 360	His	Pro	Thr	Thr	Glu 365	Met	Val	Ser
Gly	Val 370	Asn	Ile	Pro	Ala	Ala 375	Gln	Leu	Gln	Val	Ala 380	Met	Gly	Ile	Pro
Leu 385	Tyr	Ser	Ile	Arg	Asp 390	Ile	Arg	Thr	Leu	Tyr 395	Gly	Met	Asp	Pro	Arg 400
Gly	Asn	Glu	Val	Ile 405	Asp	Phe	Asp	Phe	Ser 410	Ser	Pro	Glu	Ser	Phe 415	Lys
Thr	Gln	Arg	Lys 420	Pro	Gln	Pro	Gln	Gly 425	His	Val	Val	Ala	Cys 430	Arg	Ile
Thr	Ala	Glu 435	Asn	Pro	Asp	Thr	Gly 440	Phe	Lys	Pro	Gly	Met 445	Gly	Ala	Leu
Thr	Glu 450	Leu	Asn	Phe	Arg	Ser 455	Ser	Thr	Ser	Thr	Trp 460	Gly	Tyr	Phe	Ser
Val 465	_	Thr			Ala 470	Leu				Ala 475			Gln		Gly 480
His	Ile	Phe	Ala	Tyr 485	Gly	Ala	Asp	Arg	Ser 490	Glu	Ala	Arg	Lys	Gln 495	Met
Val	Ile	Ser	Leu 500	Lys	Glu	Leu	Ser	Ile 505	Arg	Gly	Asp	Phe	Arg 510	Thr	Thr
Val	Glu	Tyr 515	Leu	Ile	Lys	Leu	Leu 520	Glu	Thr	Asp	Ala	Phe 525	Glu	Ser	Asn
Lys	Ile 530	Thr	Thr	Gly	Trp	Leu 535	Asp	Gly	Leu	Ile	Gln 540	Asp	Arg	Leu	Thr

<210> 29 <211> 539 <212> PRT <213> Ustilago maydis <220> <221> MISC FEATURE <222> (1)..(539) <223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 12-550) <400> 29 Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala 10 Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu 25 Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg 40 Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg 75 70 Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn 85 90 Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val 100 105 His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu 115 120 Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro 135 Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile

Ala Glu Arg Pro Pro

545

170

Val Ala Gln His Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly

165

Ile	Lys	Glu	Thr 180	Met	Met	Ser	Asp	Gln 185	Gly	Phe	Leu	Thr	Val 190	ser	Asp
Asp	Val	Tyr 195	Gln	Gln	Ala	Cys	Ile 200	His	Thr	Ala	Glu	Glu 205	Gly	Leu	Glu
Lys	Ala 210	Glu	Lys	Ile	Gly	Tyr 215	Pro	Val	Met	Ile	Lys 220	Ala	Ser	Glu	Gly
Gly 225	Gly	Gly	Lys	Gly	Ile 230	Arg	Lys	Cys	Thr	Asn 235	Gly	Glu	Glu	Phe	Lys 240
Gln	Leu	Tyr	Asn	Ala 245	Val	Leu	Gly	Glu	Val 250	Pro	Gly	Ser	Pro	Val 255	Phe
Val	Met	Lys	Leu 260	Alá	Gly	Gln	Ala	Arg 265	His	Leu	Glu	Val	Gln 270	Leu	Leu
Ala	Asp	Gln 275	Tyr	Gly	Asn	Ala	Ile 280	Ser	Ile	Phe	Gly	Arg 285	Asp	Cys	Ser
Val	Gln 290	Arg	Arg	His	Gln	Lys 295	Ile	Ile	Glu	Glu	Ala 300	Pro	Val	Thr	Ile
Ala 305	Pro	Glu	Asp	Ala	Arg 310	Glu	Ser	Met	Glu	Lys 315	Ala	Ala	Val	Arg	Leu 320
Ala	Lys	Leu	Val	Gly 325	Tyr	Val	Ser	Ala	Gly 330	Thr	Val	Glu	Trp	Leu 335	Tyr
Ser	Pro	Glu	Ser 340	Gly	Glu	Phe	Ala	Phe 345	Leu	Glu	Leu	Asn	Pro 350	Arg	Leu
Gln	Val	Glu 355	His	Pro	Thr	Thr	Glu 360	Met	Val	Ser	Gly	Val 365	Asn	Ile	Pro
Ala	Ala 370	Gln	Leu	Gln	Val	Ala 375	Met	Gly	Ile	Pro	Leu 380	Tyr	Ser	Ile	Arg
Asp 385	Ile	Arg	Thr	Leu	Tyr 390	Gly	Met	Asp	Pro	Arg 395	Gly	Asn	Glu	Val	Ile 400
Asp	Phe	Asp	Phe	Ser 405	Ser	Pro	Glu	Ser	Phe 410	Lys	Thr	Gln	Arg	Lys 415	Pro
Gln	Pro	Gln	Glv	His	Val	Val	Ala	Cvs	Ara	Ile	Thr	Ala	Glu	Asn	Pro

420 425 430

Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe 435 440 445

Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly 450 455 460

Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr 465 470 475 480

Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys 485 490 495

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile 500 505 510

Lys Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly 515 520 525

Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr 530 535

<210> 30

<211> 529

<212> PRT

<213> Ustilago maydis

<220>

<221> MISC\_FEATURE

<222> (1)..(529)

<223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 17-545)

<400> 30

Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys
1 5 10 15

Gln Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly
20 25 30

Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu 35 40 45

Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro 50 55 60

Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr

Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp 85 90 95

Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala 100 105 110

Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala 115 120 125

Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met 130 135 140

Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala 145 150 155 160

Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met 165 170 175

Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln 180 185 190

Ala Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile 195 200 205

Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly 210 215 220

Ile Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala 225 230 235 240

Val Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala 245 250 255

Gly Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly 260 265 270

Asn Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His 275 280 285

Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala 290 295 300

Arg Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly 305 310 315 320

Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu 

<210> 31 <211> 519 <212> PRT

Ile

- <213> Ustilago maydis
- <220>
- <221> MISC FEATURE
- <222> (1)..(519)
- <223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 22-540)
- <400> 31
- Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser

  1 10 15
- Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys 20 25 30
- Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu 35 40 45
- Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val 50 60
- Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly 65 70 75 80
- Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val 85 90 95
- Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110
- Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys 115 120 125
- Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp 130 135 140
- Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met 145 150 155 160
- Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly 165 170 175
- Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr 180 185 190
- Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met 195 200 205

IIe	Lys 210	Ala	ser	GIU	GIÀ	215	GIY	GIY	ьуѕ	GIY	220	Arg	гуѕ	Cys	1111
Asn 225	Gly	Glu	Glu	Phe	Lys 230	Gln	Leu	Tyr	Asn	Ala 235	Val	Leu	Gly	Glu	Val 240
Pro	Gly	Ser	Pro	Val 245	Phe	Val	Met	Lys	Leu 250	Ala	Gly	Gln	Ala	Arg 255	His
Leu	Glu	Val	Gln 260	Leu	Leu	Ala	Asp	Gln 265	Tyr	Gly	Asn	Ala	Ile 270	Ser	Ile
Phe	Gly	Arg 275	Asp	Cys	Ser	Val	Gln 280	Arg	Arg	His	Gln	Lys 285	Ile	Ile	Glu
Glu	Ala 290	Pro	Val	Thr	Ile	Ala 295	Pro	Glu	Asp	Ala	Arg 300	Glu	Ser	Met	Glu
Lys 305	Ala	Ala	Val	Arg	Leu 310	Ala	Lys	Leu	Val	Gly 315	Tyr	Val	Ser	Ala	Gly 320
Thr	Val	Glu	Trp	Leu 325	Tyr	Ser	Pro	Glu	Ser 330	Gly	Glu	Phe	Ala	Phe 335	Leu
Glu	Leu	Asn	Pro 340	Arg	Leu	Gln	Val	Glu 345	His	Pro	Thr	Thr	Glu 350	Met	Val
Ser	Gly	Val 355	Asn	Ile	Pro	Ala	Ala 360	Gln	Leu	Gln	Val	Ala 365	Met	Gly	Ile
Pro	Leu 370	Tyr	Ser	Ile	Arg	Asp 375	Ile	Arg	Thr	Leu	Tyr 380	Gly	Met	Asp	Pro
Arg 385	Gly	Asn	Glu	Val	Ile 390	Asp	Phe	Asp	Phe	Ser 395	Ser	Pro	Glu	Ser	Phe 400
Lys	Thr	Gln	Arg	Lys 405	Pro	Gln	Pro	Gln	Gly 410	His	Val	Val	Ala	Cys 415	Arg
Ile	Thr	Ala	Glu 420	Asn	Pro	Asp	Thr	Gly 425	Phe	Lys	Pro	Gly	Met 430	Gly	Ala
Leu	Thr	Glu 435	Leu	Asn	Phe	Arg	Ser 440	Ser	Thr	Ser	Thr	Trp 445	Gly	Tyr	Phe

Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe 450 455 460

Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln 465 470 475 480

Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr 485 490 495

Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser 500 505 510

Asn Lys Ile Thr Thr Gly Trp 515

<210> 32

<211> 580

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC\_FEATURE

<222> (76)..(76)

<223> Saccharomyces cerevisiae ACCase BC domain S77Y mutation

<400> 32

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu 1 5 10 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile 20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe 35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Tyr Val Arg Lys Trp 65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met 85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala 100 105 110

Asp	Gln	Tyr 115	Ile	Glu	Val	Pro	120	GIA	Thr	Asn	Asn	125	ASI	Tyr	Ala
Asn	Val 130	Asp	Leu	Ile	Val	Asp 135	Ile	Ala	Glu	Arg	Ala 140	Asp	Val	Asp	Ala
Val 145	Trp	Ala	Gly	Trp	Gly 150	His	Ala	Ser	Glu	Asn 155	Pro	Leu	Leu	Pro	Glu 160
Lys	Leu	Ser	Gln	Ser 165	Lys	Arg	Lys	Val	Ile 170	Phe	Ile	Gly	Pro	Pro 175	Gly
Asn	Ala	Met	Arg 180	Ser	Leu	Gly	Asp	Lys 185	Ile	Ser	Ser	Thr	Ile 190	Val	Ala
Gln	Ser	Ala 195	Lys	Val	Pro	Cys	Ile 200	Pro	Trp	Ser	Gly	Thr 205	Gly	Val	Asp
Thr	Val 210	His	Val	Asp	Glu	Lys 215	Thr	Gly	Leu	Val	Ser 220	Val	Asp	Asp	Asp
Ile 225	Tyr	Gln	Lys	Gly	Cys 230	Cys	Thr	Ser	Pro	Glu 235	Asp	Gly	Leu	Gln	Lys 240
Ala	Lys	Arg	Ile	Gly 245	Phe	Pro	Val	Met	Ile 250	Lys	Ala	Ser	Glu	Gly 255	Gly
Gly	Gly	Lys	Gly 260	Ile	Arg	Gln	Val	Glu 265	Arg	Glu	Glu	Asp	Phe 270	Ile	Ala
Leu	Tyr	His 275	Gln	Ala	Ala	Asn	Glu 280	Ile	Pro	Gly	Ser	Pro 285	Ile	Phe	Ile
Met	Lys 290	Leu	Ala	Gly	Arg	Ala 295	Arg	His	Leu	Glu	Val 300	Gln	Leu	Leu	Ala
Asp 305	Gln	Tyr	Gly	Thr	Asn 310	Ile	Ser	Leu	Phe	Gly 315	Arg	Asp	Cys	Ser	Val 320
Gln	Arg	Arg	His	Gln 325	Lys	Ile	Ile	Glu	Glu 330	Ala	Pro	Val	Thr	Ile 335	Ala
Lys	Ala	Glu	Thr 340	Phe	His	Glu	Met	Glu 345	Lys	Ala	Ala	Val	Arg 350	Leu	Gly
Tara	T 011	Val.	C117	ጥ፣ ፣ ጉ	v-1	Car	7 T =	Gly	Thr	Val	Glu	Tur	T.e.11	Tvr	Ser

355 360 365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln 370 375 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala 385 390 395 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp 405 410 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp 420 425 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile 435 440 445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn 450 455 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu 515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 530 540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp 545 550 555 560

Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro 565 570 575

Thr Leu Ala Val 580

<210> 33 <211> 575

- <212> PRT
- <213> Saccharomyces cerevisiae
- <220>
- <221> MISC FEATURE
- <222> (1)..(575)
- <223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 7-581)
- <400> 33
- Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser 1 5 10 15
- Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val 20 25 30
- Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly 35 40 45
- Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala 50 55 60
- Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe 65 70 75 80
- Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp 85 90 95
- Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu 100 105 110
- Val Pro Gly Gly Thr Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile 115 120 125
- Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp 130 135 140
- Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser 145 150 155 160
- Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser 165 170 175
- Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val
  180 185 190
- Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp

195	200	205

Glu	Lys 210	Thr	Gly	Leu	Val	Ser 215	Val	Asp	Asp	Asp	Ile 220	Tyr	Gln	Lys	Gly
Cys 225	Cys	Thr	Ser	Pro	Glu 230	Asp	Gly	Leu	Gln	Lys 235	Ala	Lys	Arg	Ile	Gly 240
Phe	Pro	Val	Met	Ile 245	Lys	Ala	Ser	Glu	Gly 250	Gly	Gly	Gly	Lys	Gly 255	Ile
Arg	Gln	Val	Glu 260	Arg	Glu	Glu	Asp	Phe 265	Ile	Ala	Leu	Tyr	His 270	Gln	Ala
Ala	Asn	Glu 275	Ile	Pro	Gly	Ser	Pro 280	Ile	Phe	Ile	Met	Lys 285	Leu	Ala	Gly
Arg	Ala 290	Arg	His	Leu	Glu	Val 295	Gln	Leu	Leu	Ala	Asp 300	Gln	Tyr	Gly	Thr
Asn 305	Ile	Ser	Leu	Phe	Gly 310	Arg	Asp	Cys	Ser	Val 315	Gln	Arg	Arg	His	Gln 320
Lys	Ile	Ile	Glu	Glu 325	Ala	Pro	Val	Thr	Ile 330	Ala	Lys	Ala	Glu	Thr 335	Phe
His	Glu	Met	Glu 340	Lys	Ala	Ala	Val	Arg 345	Leu	Gly	Lys	Leu	Val 350	Gly	Tyr
Val	Ser	Ala 355	Gly	Thr	Val	Glu	Tyr 360	Leu	Tyr	Ser	His	Asp 365	Asp	Gly	Lys
Phe	Tyr 370	Phe	Leu	Glu	Leu	Asn 375	Pro	Arg	Leu	Gln	Val 380	Glu	His	Pro	Thr
Thr 385	Glu	Met	Val	Ser	Gly 390	Val	Asn	Leu	Pro	Ala 395	Ala	Gln	Leu	Gln	Ile 400
Ala	Met	Gly	Ile	Pro 405	Met	His	Arg	Ile	Ser 410	Asp	Ile	Arg	Thr	Leu 415	Tyr
Gly	Met	Asn	Pro 420	His	Ser	Ala	Ser	Glu 425	Ile	Asp	Phe	Glu	Phe 430	Lys	Thr
Gln	Asp	Ala 435	Thr	Lys	Lys	Gln	Arg 440	Arg	Pro	Ile	Pro	Lys 445	Gly	His	Cys

Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro 450 455 460

Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val 465 470 475 480

Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser 485 490 495

Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala
500 505 510

Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly 515 520 525

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu 530 540

Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile 545 550 555

Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val 565 570 575

<210> 34

<211> 570

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC FEATURE

<222> (1)..(570)

<223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 12-581)

<400> 34

Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu 1 5 10 15

Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu 20 25 30

Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile 35 40 45

Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile

Arg	Ser	Val	Arg	Lys	Trp	Ala	Tyr	Glu	Thr	Phe	Gly	Asp	Asp	Arg	Thr
65					70					75					80

Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala 

Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr

Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu 

Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu

Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile 

Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile 

Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp 

Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu 

Val Ser Val Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro 

Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile 

Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg 

Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro 

Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu 

Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe 

Gly 305	Arg	Asp	Cys	Ser	Val 310	Gln	Arg	Arg	His	Gln 315	Lys	Ile	Ile	Glu	Glu 320
Ala	Pro	Val	Thr	Ile 325	Ala	Lys	Ala	Glu	Thr 330	Phe	His	Glu	Met	Glu 335	Lys
Ala	Ala	Val	Arg 340	Leu	Gly	Lys	Leu	Val 345	Gly	Tyr	Val	Ser	Ala 350	Gly	Thr
Val	Glu	Tyr 355	Leu	Tyr	Ser	His	Asp 360	Asp	Gly	Lys	Phe	Tyr 365	Phe	Leu	Glu
Leu	Asn 370	Pro	Arg	Leu	Gln	Val 375	Glu	His	Pro	Thr	Thr 380	Glu	Met	Val	Ser
Gly 385	Val	Asn	Leu	Pro	Ala 390	Ala	Gln	Leu	Gln	Ile 395	Ala	Met	Gly	Ile	Pro 400
Met	His	Arg	Ile	Ser 405	Asp	Ile	Arg	Thr	Leu 410	Tyr	Gly	Met	Asn	Pro 415	His
Ser	Ala	Ser	Glu 420	Ile	Asp	Phe	Glu	Phe 425	Lys	Thr	Gln	Asp	Ala 430	Thr	Lys
Lys	Gln	Arg 435	Arg	Pro	Ile	Pro	Lys 440	Gly	His	Cys	Thr	Ala 445	Cys	Arg	Ile
Thr	Ser 450	Glu	Asp	Pro	Asn	Asp 455	Gly	Phe	Lys	Pro	Ser 460	Gly	Gly	Thr	Leu
His 465	Glu	Leu	Asn	Phe	Arg 470	Ser	Ser	Ser	Asn	Val 475	Trp	Gly	Tyr	Phe	Ser 480
Val	Gly	Asn	Asn	Gly 485	Asn	Ile	His	Ser	Phe 490	Ser	Asp	Ser	Gln	Phe 495	Gly
His	Ile	Phe	Ala 500	Phe	Gly	Glu	Asn	Arg 505	Gln	Ala	Ser	Arg	Lys 510	His	Met
Val	Val	Ala 515	Leu	Lys	Glu	Leu	Ser 520	Ile	Arg	Gly	Asp	Phe 525	Arg	Thr	Thr
Val	Glu 530	Tyr	Leu	Ile	Lys	Leu 535	Leu	Glu	Thr	Glu	Asp 540	Phe	Glu	Asp	Asn

Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr 545 550 550 560

Ala Glu Lys Pro Asp Pro Thr Leu Ala Val 565 570

- <210> 35
- <211> 560
- <212> PRT
- <213> Saccharomyces cerevisiae
- <220>
- <221> MISC FEATURE
- <222> (1)..(560)
- <223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 22-581)
- <400> 35
- Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr 1 5 10 15
- Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His 20 25 30
- Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile 35 40 45
- Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr 50 55 60
- Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu 65 70 75 80
- Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile 85 90 95
- Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu 100 105 110
- Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly 115 120 125
- Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln 130 135 140
- Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg 145 150 155 160

Ser	Leu	Gly	Asp	Lys 165	Ile	Ser	Ser	Thr	Ile 170	Val	Ala	Gln	Ser	Ala 175	Lys
Val	Pro	Cys	Ile 180	Pro	Trp	Ser	Gly	Thr 185	Gly	Val	Asp	Thr	Val 190	His	Val
Asp	Glu	Lys 195	Thr	Gly	Leu	Val	Ser 200	Val	Asp	Asp	Asp	Ile 205	Tyr	Gln	Lys
Gly	Cys 210	Cys	Thr	Ser	Pro	Glu 215	Asp	Gly	Leu	Gln	Lys 220	Ala	Lys	Arg	Ile
Gly 225	Phe	Pro	Val	Met	Ile 230	Lys	Ala	Ser	Glu	Gly 235	Gly	Gly	Gly	Lys	Gly 240
Ile	Arg	Gln	Val	Glu 245	Arg	Glu	Glu	Asp	Phe 250	Ile	Ala	Leu	Tyr	His 255	Gln
Ala	Ala	Asn	Glu 260	Ile	Pro	Gly	Ser	Pro 265	Ile	Phe	Ile	Met	Lys 270	Leu	Ala
Gly	Arg	Ala 275	Arg	His	Leu	Glu	Val 280	Gln	Leu	Leu	Ala	Asp 285	Gln	Tyr	Gly
Thr	Asn 290	Ile	Ser	Leu	Phe	Gly 295	Arg	Asp	Cys	Ser	Val 300	Gln	Arg	Arg	His
Gln 305	Lys	Ile	Ile	Glu	Glu 310	Ala	Pro	Val	Thr	Ile 315	Ala	Lys	Ala	Glu	Thr 320
Phe	His	Glu	Met	Glu 325	Lys	Ala	Ala	Val	Arg 330	Leu	Gly	Lys	Leu	Val 335	Gly
Tyr	Val	Ser	Ala 340	Gly	Thr	Val	Glu	Tyr 345	Leu	Tyr	Ser	His	Asp 350	Asp	Gly
Lys	Phe	Tyr 355	Phe	Leu	Glu	Leu	Asn 360	Pro	Arg	Leu	Gln	Val 365	Glu	His	Pro
Thr	Thr 370	Glu	Met	Val	Ser	Gly 375	Val	Asn	Leu	Pro	Ala 380	Ala	Gln	Leu	Gln
Ile 385	Ala	Met	Gly	Ile	Pro 390	Met	His	Arg	Ile	Ser 395	Asp	Ile	Arg	Thr	Leu 400

Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His 425 Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys 440 Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Asn 455 Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe 470 475 Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln 490 Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg 500 505 Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr 515 520 Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu 535 Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val 550 555 <210> 36 <211> 550 <212> PRT <213> Saccharomyces cerevisiae <220> <221> MISC\_FEATURE (1)..(550) <222> <223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 32-581 <400> 36 Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg

30

Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu

25

20

- Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg 35 40 45
- Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val 50 55 60
- Ala Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg 65 70 75 80
- Met Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn 85 90 95
- Tyr Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val 100 105 110
- Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu 115 120 125
- Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro 130 135 140
- Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile 145 150 155 160
- Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly
  165 170 175
- Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp 180 185 190
- Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu 195 200 205
- Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu 210 215 220
- Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe 225 230 235 240
- Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile 245 250 255
- Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu 260 265 270

Leu	Ala	Asp 275	Gln	Tyr	Gly	Thr	Asn 280	Ile	Ser	Leu	Phe	Gly 285	Arg	Asp	Cys
Ser	Val 290	Gln	Arg	Arg	His	Gln 295	Lys	Ile	Ile	Glu	Glu 300	Ala	Pro	Val	Thr
Ile 305	Ala	Lys	Ala	Glu	Thr 310	Phe	His	Glu	Met	Glu 315	Lys	Ala	Ala	Val	Arg 320
Leu	Gly	Lys	Leu	Val 325	Gly	Tyr	Val	Ser	Ala 330	Gly	Thr	Val	Glu	Tyr 335	Leu
Tyr	Ser	His	Asp 340	Asp	Gly	Lys	Phe	Tyr 345	Phe	Leu	Glu	Leu	Asn 350	Pro	Arg
Leu	Gln	Val 355	Glu	His	Pro	Thr	Thr 360	Glu	Met	Val	Ser	Gly 365	Val	Asn	Leu
Pro	Ala 370	Ala	Gln	Leu	Gln	Ile 375	Ala	Met	Gly	Ile	Pro 380	Met	His	Arg	Ile
Ser 385	Asp	Ile	Arg	Thr	Leu 390	Tyr	Gly	Met	Asn	Pro 395	His	Ser	Ala	Ser	Glu 400
Ile	Asp	Phe	Glu	Phe 405	Lys	Thr	Gln	Asp	Ala 410	Thr	Lys	Lys	Gln	Arg 415	Arg
Pro	Ile	Pro	Lys 420	Gly	His	Cys	Thr	Ala 425	Cys	Arg	Ile	Thr	Ser 430	Glu	Asp
Pro	Asn	Asp 435	Gly	Phe	Lys	Pro	Ser 440	Gly	Gly	Thr	Leu	His 445	Glu	Leu	Asn
Phe	Arg 450	Ser	Ser	Ser	Asn	Val 455	Trp	Gly	Tyr	Phe	Ser 460	Val	Gly	Asn	Asn
Gly 465	Asn	Ile	His	Ser	Phe 470	Ser	Asp	Ser	Gln	Phe 475	Gly	His	Ile	Phe	Ala 480
Phe	Gly	Glu	Asn	Arg 485	Gln	Ala	Ser	Arg	Lys 490	His	Met	Val	Val	Ala 495	Leu
Lys	Glu	Leu	Ser 500	Ile	Arg	Gly	Asp	Phe 505	Arg	Thr	Thr	Val	Glu 510	Tyr	Leu

- Ile Lys Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr
  515 520 525
- Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro 530 540

Asp Pro Thr Leu Ala Val 545 550

- <210> 37
- <211> 540
- <212> PRT
- <213> Saccharomyces cerevisiae
- <220>
- <221> MISC FEATURE
- <222> (1)..(540)
- <223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 42-581)
- <400> 37
- Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr 1 5 10 15
- Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys
  20 25 30
- Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp 35 40 45
- Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu Ala 50 60
- Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro Gly 65 70 75 80
- Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile 85 90 95
- Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110
- Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys 115 120 125
- Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp 130 135 140

Lys 145	Ile	Ser	Ser	Thr	Ile 150	Val	Ala	Gln	Ser	Ala 155	Lys	Val	Pro	Cys	Ile 160
Pro	Trp	Ser	Gly	Thr 165	Gly	Val	Asp	Thr	Val 170	His	Val	Asp	Glu	Lys 175	Thr
Gly	Leu	Val	Ser 180	Val	Asp	Asp	Asp	Ile 185	Tyr	Gln	Lys	Gly	Cys 190	Cys	Thr
Ser	Pro	Glu 195	Asp	Gly	Leu	Gln	Lys 200	Ala	Lys	Arg	Ile	Gly 205	Phe	Pro	Val
Met	Ile 210	Lys	Ala	Ser	Glu	Gly 215	Gly	Gly	Gly	Lys	Gly 220	Ile	Arg	Gln	Val
Glu 225	Arg	Glu	Glu	Asp	Phe 230	Ile	Ala	Leu	Tyr	His 235	Gln	Ala	Ala	Asn	Glu 240
Ile	Pro	Gly	Ser	Pro 245	Ile	Phe	Ile	Met	Lys 250	Leu	Ala	Gly	Arg	Ala 255	Arg
His	Leu	Glu	Val 260	Gln	Leu	Leu	Ala	Asp 265	Gln	Tyr	Gly	Thr	Asn 270	Ile	Ser
Leu	Phe	Gly 275	Arg	Asp	Cys	Ser	Val 280	Gln	Arg	Arg	His	Gln 285	Lys	Ile	Ile
Glu	Glu 290	Ala	Pro	Val	Thr	Ile 295	Ala	Lys	Ala	Glu	Thr 300	Phe	His	Glu	Met
Glu 305	Lys	Ala	Ala	Val	Arg 310	Leu	Gly	Lys	Leu	Val 315	Gly	Tyr	Val	Ser	Ala 320
Gly	Thr	Val	Glu	Tyr 325	Leu	Tyr	Ser	His	Asp 330	Asp	Gly	Lys	Phe	Tyr 335	Phe
Leu	Glu	Leu	Asn 340	Pro	Arg	Leu	Gln	Val 345	Glu	His	Pro	Thr	Thr 350	Glu	Met
Val	Ser	Gly 355	Val	Asn	Leu	Pro	Ala 360	Ala	Gln	Leu	Gln	Ile 365	Ala	Met	Gly
Ile	Pro 370	Met	His	Arg	Ile	Ser 375	Asp	Ile	Arg	Thr	Leu 380	Tyr	Gly	Met	Asn

Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala 385 390 395 400	
Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala Cys 405 410 415	
Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly 420 425 430	
Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr 435 440 445	
Phe Ser Val Gly Asn Gly Asn Ile His Ser Phe Ser Asp Ser Gln 450 455 460	
Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys 465 470 475 480	
His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg 485 490 495	
Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu 500 505 510	
Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His Lys 515 520 525	
Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val 530 535 540	
<210> 38 <211> 575 <212> PRT <213> Saccharomyces cerevisiae	
<220> <221> MISC_FEATURE <222> (1)(575) <223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AA 2-576)	.s
<400> 38	
Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu 1 5 10 15	
Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile 20 25 30	

Gly Leu Asn 35	Thr Val	Asp Lys	Leu G 40	lu Glu	Ser Pro	Leu Arg 45	Asp	Phe
Val Lys Ser 50	His Gly	Gly His 55	Thr V	al Ile	Ser Lys 60	Ile Leu	Ile	Ala
Asn Asn Gly 65	Ile Ala	Ala Val 70	Lys G	lu Ile	Arg Ser 75	Val Arg	Lys	Trp 80
Ala Tyr Glu	Thr Phe 85	Gly Asp	Asp A	arg Thr 90	Val Gln	Phe Val	Ala 95	Met
Ala Thr Pro	Glu Asp 100	Leu Glu		sn Ala .05	Glu Tyr	Ile Arg		Ala
Asp Gln Tyr 115		Val Pro	Gly G 120	ly Thr	Asn Asn	Asn Asn 125	Tyr	Ala
Asn Val Asp 130	Leu Ile	Val Asp 135		ala Glu	Arg Ala 140	Asp Val	Asp	Ala
Val Trp Ala 145	Gly Trp	Gly His	Ala S	Ser Glu	Asn Pro 155	Leu Leu	Pro	Glu 160
Lys Leu Ser	Gln Ser 165		Lys V	al Ile 170	Phe Ile	Gly Pro	Pro 175	Gly
Asn Ala Met	Arg Ser 180	Leu Gly	_	ys Ile .85	Ser Ser	Thr Ile		Ala
Gln Ser Ala 195	-	Pro Cys	Ile P 200	ro Trp	Ser Gly	Thr Gly 205	Val	Asp
Thr Val His	Val Asp	Glu Lys 215		ly Leu	Val Ser 220	Val Asp	Asp	Asp
Ile Tyr Gln 225	Lys Gly	Cys Cys 230	Thr S	Ser Pro	Glu Asp 235	Gly Leu	Gln	Lys 240
Ala Lys Arg	Ile Gly 245		Val M	Met Ile 250	Lys Ala	Ser Glu	Gly 255	Gly
Gly Gly Lys	Gly Ile 260	Arg Gln		lu Arg	Glu Glu	Asp Phe		Ala

Leu	Tyr	His 275	Gln	Ala	Ala	Asn	Glu 280	Ile	Pro	Gly	Ser	Pro 285	Ile	Phe	Ile
Met	Lys 290	Leu	Ala	Gly	Arg	Ala 295	Arg	His	Leu	Glu	Val 300	Gln	Leu	Leu	Ala
Asp 305	Gln	Tyr	Gly	Thr	Asn 310	Ile	Ser	Leu	Phe	Gly 315	Arg	Asp	Cys	Ser	Val 320
Gln	Arg	Arg	His	Gln 325	Lys	Ile	Ile	Glu	Glu 330	Ala	Pro	Val	Thr	Ile 335	Ala
Lys	Ala	Glu	Thr 340	Phe	His	Glu	Met	Glu 345	Lys	Ala	Ala	Val	Arg 350	Leu	Gly
Lys	Leu	Val 355	Gly	Tyr	Val	Ser	Ala 360	Gly	Thr	Val	Glu	Tyr 365	Leu	Tyr	Ser
His	Asp 370	Asp	Gly	Lys	Phe	Tyr 375	Phe	Leu	Glu	Leu	Asn 380	Pro	Arg	Leu	Gln
Val 385	Glu	His	Pro	Thr	Thr 390	Glu	Met	Val	Ser	Gly 395	Val	Asn	Leu	Pro	Ala 400
Ala	Gln	Leu	Gln	Ile 405		Met	Gly	Ile	Pro 410	Met	His	Arg	Ile	Ser 415	Asp
Ile	Arg	Thr	Leu 420	Tyr	Gly	Met	Asn	Pro 425	His	Ser	Ala	Ser	Glu 430	Ile	Asp
Phe	Glu	Phe 435	Lys	Thr	Gln	Asp	Ala 440	Thr	Lys	Lys	Gln	Arg 445	Arg	Pro	Ile
Pro	Lys 450	Gly	His	Cys	Thr	Ala 455	Cys	Arg	Ile	Thr	Ser 460	Glu	Asp	Pro	Asn
Asp 465	Gly	Phe	Lys	Pro	Ser 470	Gly	Gly	Thr	Leu	His 475	Glu	Leu	Asn	Phe	Arg 480
Ser	Ser	Ser	Asn	Val 485	Trp	Gly	Tyr	Phe	Ser 490	Val	Gly	Asn	Asn	Gly 495	Asn
Ile	His	Ser	Phe 500	Ser	Asp	Ser	Gln	Phe 505	Gly	His	Ile	Phe	Ala 510	Phe	Gly
Glu	Asn	Arg	Gln	Ala	Ser	Arg	Lys	His	Met	Val	Val	Ala	Leu	Lys	Glu

520 525 515

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 535 530

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp 550 555

Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp 565 570

<210> 39

<211> 570 <212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC\_FEATURE

<222> (1)..(570)

<223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 2-571)

<400> 39

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile 25

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 55

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met 85 90

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala 100 105

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala 125 115 120

Asn	Val 130	Asp	Leu	Ile	Val	Asp 135	Ile	Ala	Glu	Arg	Ala 140	Asp	Val	Asp	Ala
Val 145	Trp	Ala	Gly	Trp	Gly 150	His	Ala	Ser	Glu	Asn 155	Pro	Leu	Leu	Pro	Glu 160
Lys	Leu	Ser	Gln	Ser 165	Lys	Arg	Lys	Val	Ile 170	Phe	Ile	Gly	Pro	Pro 175	Gly
Asn	Ala	Met	Arg 180	Ser	Leu	Gly	Asp	Lys 185	Ile	Ser	Ser	Thr	Ile 190	Val	Ala
Gln	Ser	Ala 195	Lys	Val	Pro	Cys	Ile 200	Pro	Trp	Ser	Gly	Thr 205	Gly	Val	Asp
Thr	Val 210	His	Val	Asp	Glu	Lys 215	Thr	Gly	Leu	Val	Ser 220	Val	Asp	Asp	Asp
Ile 225	Tyr	Gln	Lys	Gly	Cys 230	Cys	Thr	Ser	Pro	Glu 235	Asp	Gly	Leu	Gln	Lys 240
Ala	Lys	Arg	Ile	Gly 245	Phe	Pro	Val	Met	Ile 250	Lys	Ala	Ser	Glu	Gly 255	Gly
Gly	Gly	Lys	Gly 260	Ile	Arg	Gln	Val	Glu 265	Arg	Glu	Glu	Asp	Phe 270	Ile	Ala
Leu	Tyr	His 275	Gln	Ala	Ala	Asn	Glu 280	Ile	Pro	Gly	Ser	Pro 285	Ile	Phe	Ile
Met	Lys 290	Leu	Ala	Gly	Arg	Ala 295	Arg	His	Leu	Glu	Val 300	Gln	Leu	Leu	Ala
Asp 305	Gln	Tyr	Gly	Thr	Asn 310	Ile	Ser	Leu	Phe	Gly 315	Arg	Asp	Cys	Ser	Val 320
Gln	Arg	Arg	His	Gln 325	Lys	Ile	Ile	Glu	Glu 330	Ala	Pro	Val	Thr	Ile 335	Ala
Lys	Ala	Glu	Thr 340	Phe	His	Glu	Met	Glu 345	Lys	Ala	Ala	Val	Arg 350	Leu	Gly
Lys	Leu	Val 355	Gly	Tyr	Val	Ser	Ala 360	Gly	Thr	Val	Glu	Tyr 365	Leu	Tyr	Ser
His	Asp	Asp	Gly	Lys	Phe	Tyr	Phe	Leu	Glu	Leu	Asn	Pro	Arg	Leu	Gln

370 375 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala 385 390 395 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp 405 410 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp 420 425 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Pro Ile 435 440 445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn 450 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu 515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 530 535 540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp 545 550 555 560

Leu Asp Asp Leu Ile Thr His Lys Met Thr 565 570

<210> 40

<211> 560

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC\_FEATURE

<222> (1)..(560)

<223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs

2-561)

<400> 40

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu 1 5 10 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile
20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe 35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp 65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met 85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala 100 105 110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala 115 120 125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala 130 135 140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu 145 150 155 160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly
165 170 175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala 180 185 190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp 195 200 205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp 210 215 220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys

225	230	235	240

Ala Lys Ar	g Ile G	ly Phe	Pro	Val	Met	Ile	Lys	Ala	Ser	Glu	Gly	Gly
	2	45				250					255	

- Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala 260 265 270
- Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile 275 280 285
- Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala 290 295 300
- Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val 305 310 315 320
- Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala 325 330 335
- Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly 340 345 350
- Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser 355 360 365
- His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln 370 375 380
- Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala 385 390 395 400
- Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp 405 410 415
- Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp 420 425 430
- Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile 435 440 445
- Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn 450 455 460
- Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu 515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 530 535

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp 545 550 555 560

<210> 41

<211> 550

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC FEATURE

<222> (1)..(550)

<223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 2-551)

<400> 41

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu 1 5 10 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile 20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe
35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 50 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp 65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala

100	105	110

Asp	Gln	Tyr	Ile	Glu	Val	Pro	Gly	Gly	Thr	Asn	Asn	Asn	Asn	Tyr	Ala
		115					120					125		_	

- Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala
  130 140
- Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu 145 150 155 160
- Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly
  165 170 175
- Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala 180 185 190
- Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp 195 200 205
- Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp 210 215 220
- Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys 225 230 235 240
- Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly 245 250 255
- Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala 260 265 270
- Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile 275 280 285
- Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala 290 295 300
- Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val 305 310 315 320
- Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala 325 330 335
- Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly 340 345 350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser 355 360 365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln 370 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala 385 390 395 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp 405 410 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp 420 425 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile 435 440 445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn 450 455 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly
500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu
515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 530 535 540

Leu Leu Glu Thr Glu Asp 545 550

<210> 42

<211> 540

<212> PRT

<213> Saccharomyces cerevisiae

<220>

- <221> MISC\_FEATURE <222> (1)..(540) <223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 2-541)

<400> 42

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile 20

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe 40

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 50 55

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala 100

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala 120

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu 155

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly 170

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala 185

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp 200

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp 215 220

225	i Tyr	c Gli	n Lys	s Gly	230	Cys	5 Thi	Ser	r Pro	235		o Gly	y Lei	ı Glı	Lys 240
Ala	Lys	arç	g Ile	e Gly 245	Phe	Pro	Val	. Met	: Ile 250		s Ala	a Sei	r Glı	1 Gly 259	y Gly
Gly	Gly	r Lys	3 Gly 260	r Ile	Arg	Gln	ı Val	. Glu 265		g Glu	ı Glu	ı As <u>r</u>	270		e Ala
Leu	Tyr	His 275	s Gln	Ala	Ala	Asn	Glu 280		Pro	Gly	Ser	285		Ph∈	e Ile
Met	Lys 290	Leu	ı Ala	Gly	Arg	Ala 295	Arg	His	Leu	Glu	Val 300		ı Leu	Lev	ı Ala
Asp 305	Gln	Tyr	Gly	Thr	Asn 310	Ile	Ser	Leu	Phe	Gly 315		Asp	Cys	Ser	Val 320
Gln	Arg	Arg	His	Gln 325	Lys	Ile	Ile	Glu	Glu 330	Ala	Pro	Val	Thr	Ile 335	Ala
Lys	Ala	Glu	Thr 340	Phe	His	Glu	Met	Glu 345	Lys	Ala	Ala	Val	Arg 350	Leu	Gly
Lys	Leu	Val 355	Gly	Tyr	Val	Ser	Ala 360	Gly	Thr	Val	Glu	Tyr 365	Leu	Tyr	Ser
His	Asp 370	Asp	Gly	Lys	Phe	Tyr 375	Phe	Leu	Glu	Leu	Asn 380	Pro	Arg	Leu	Gln
Val 385	Glu	His	Pro	Thr	Thr 390	Glu	Met	Val	Ser	Gly 395	Val	Asn	Leu	Pro	Ala 400
Ala	Gln	Leu	Gln	Ile 405	Ala	Met	Gly	Ile	Pro 410	Met	His	Arg	Ile	Ser 415	Asp
Ile	Arg	Thr	Leu 420	Tyr	Gly	Met	Asn	Pro 425	His	Ser	Ala	Ser	Glu 430	Ile	Asp
Phe	Glu	Phe 435	Lys	Thr	Gln	Asp	Ala 440	Thr	Lys	Lys		Arg 445	Arg	Pro	Ile
Pro	Lys 450	Gly	His	Cys	Thr	Ala 455	Cys	Arg	Ile		Ser 460	Glu	Asp	Pro	Asn

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg 465 470

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn 485

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly 500

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu 515 520

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu 530 535

<210> 43

<211> 575 <212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC\_FEATURE

<222> (1). (575) <223> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 4-578)

<400> 43

Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr 5 10

Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu 20

Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys

Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn

Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr 70 75

Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr 85 90

Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln 100 105 110

Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala

Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Tyr Ala Asn Val

Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu

- Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp 355 360
- Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu 370 375
- His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln
- Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg
- Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu 420
- Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys 435 440
- Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly 450 455
- Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser 465 470 475
- Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His 485 490
- Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn 500 505
- Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser 515 520 525
- Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu 530 535
- Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp 545 550
- Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr 565 570

- <210> 44 <211> 570 <212> PRT <213> Saccharomyces cerevisiae

<220>

<221> MISC FEATURE

<222> (1)..(570)

<223> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 7-576)

<400> 44

Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser 1 5 10 15

Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val 20 25 30

Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly 35 40 45

Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala 50 55 60

Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe 65 70 75 80

Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp 85 90 95

Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu 100 105 110

Val Pro Gly Gly Thr Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile 115 120 125

Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp 130 135 140

Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser 145 150 155 160

Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser 165 170 175

Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val 180 185 190

Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp 195 200 205

210 215 Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly 225 230 235 Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile 245 250 Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala 265 Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly 275 280 Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr 290 Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln 305 310 Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe 325 His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr 340 Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys 355 360 Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr 370 Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile 390 395 Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr 410

Glu Lys Thr Gly Leu Val Ser Val Asp Asp Ile Tyr Gln Lys Gly

Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr

Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys
435

Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro 450 450 460

Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val 465 470 475 480

Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser 485 490 495

Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala 500 505 510

Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly 515 520 525

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu 530 540

Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile 545 550 555 560

Thr His Lys Met Thr Ala Glu Lys Pro Asp 565 570

<210> 45

<211> 560

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC\_FEATURE

<222> (1)..(560)

<223> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 12-571)

<400> 45

Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu 1 5 10 15

Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu 20 25 30

Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile 35 40 45

Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile 50 55 60

- Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr 65 70 75 80
- Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala 85 90 95
- Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr 100 105 110
- Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu 115 120 125
- Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu 130 135 140
- Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile 145 150 155 160
- Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile 165 170 175
- Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp 180 185 190
- Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu 195 200 205
- Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro 210 215 220
- Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile 225 230 235 240
- Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg
  245 250 255
- Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro 260 265 270
- Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu 275 280 285
- Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe 290 295 300

305		ASP	, cys	Ser	310		ALG	Arg	nis	315	_	3 116	: 116	e GIU	320
Ala	Pro	Val	Thr	Ile 325		Lys	Ala	. Glu	Thr 330		His	: Glu	ı Met	: Glu 335	ı Lys
Ala	Ala	Val	Arg 340		Gly	Lys	Leu	Val 345		Туг	Val	. Ser	350		Thr
Val	Glu	Tyr 355		Tyr	Ser	His	Asp 360		Gly	· Lys	Phe	Tyr 365		e Leu	Glu
Leu	Asn 370		Arg	Leu	Gln	Val 375		His	Pro	Thr	Thr 380		. Met	. Val	Ser
Gly 385		Asn	Leu	Pro	Ala 390	Ala	Gln	Leu	Gln	Ile 395		Met	Gly	lle	Pro 400
Met	His	Arg	Ile	Ser 405	Asp	Ile	Arg	Thr	Leu 410	Tyr	Gly	Met	Asn '	Pro 415	His
Ser	Ala	Ser	Glu 420	Ile	Asp	Phe	Glu	Phe 425	Lys	Thr	Gln	Asp	Ala 430		Lys
Lys	Gln	Arg 435	Arg	Pro	Ile	Pro	Lys 440	Gly	His	Cys	Thr	Ala 445	Cys	Arg	Ile
Thr	Ser 450	Glu	Asp	Pro	Asn	Asp 455	Gly	Phe	Lys	Pro	Ser 460	Gly	Gly	Thr	Leu
His 465	Glu	Leu	Asn	Phe	Arg 470	Ser	Ser	Ser	Asn	Val 475	Trp	Gly	Tyr	Phe	Ser 480
Val	Gly	Asn	Asn	Gly 485	Asn	Ile	His	Ser	Phe 490	Ser	Asp	Ser	Gln	Phe 495	Gly
His	Ile	Phe	Ala 500	Phe	Gly	Glu	Asn	Arg 505	Gln	Ala	Ser	Arg	Lys 510	His	Met
Val	Val	Ala 515	Leu	Lys	Glu	Leu	Ser 520	Ile	Arg	Gly	Asp	Phe 525	Arg	Thr	Thr
Val	Glu 530	Tyr	Leu	Ile	Lys	Leu 535	Leu	Glu	Thr	Glu	Asp 540	Phe	Glu	Asp	Asn
Thr	Ile	Thr	Thr	Gly	Trp	Leu	Asp	Asp	Leu	Ile	Thr	His	Lys	Met	Thr

<210> 46

<211> 550

<212> PRT <213> Saccharomyces cerevisiae

<220>

<221> MISC\_FEATURE

<222> (1). (550) <223> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 17-566)

<400> 46

Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe 5

Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp 20

Phe Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile 35 40

Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys

Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala

Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met 85

Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Tyr 100 105

Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro 135

Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro 150 155

Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val 165 170

Ala Gln Se	er Ala Lys 180	: Val Pro	Cys Il 18	-	Ser Gly	Thr Gly 190	Val
Asp Thr Va		. Asp Glu	Lys Th 200	r Gly Leu	Val Ser 205	_	Asp
Asp Ile Ty 210	r Gln Lys	Gly Cys 215	_	r Ser Pro	Glu Asp 220	Gly Leu	Gln
Lys Ala Ly 225	vs Arg Ile	e Gly Phe 230	Pro Va	l Met Ile 235	-	Ser Glu	Gly 240
Gly Gly G	y Lys Gly 245	_	Gln Va	l Glu Arg 250	Glu Glu	Asp Phe 255	
Ala Leu Ty	r His Glr 260	n Ala Āla	Asn Gl 26		Gly Ser	Pro Ile 270	Phe
Ile Met Ly 27		Gly Arg	Ala Ar 280	g His Leu	Glu Val 285		Leu
Ala Asp Gl 290	n Tyr Gly	Thr Asn 295		r Leu Phe	Gly Arg 300	Asp Cys	Ser
Val Gln Ar 305	g Arg His	Gln Lys 310	Ile Il	e Glu Glu 315	Ala Pro	Val Thr	Ile 320
Ala Lys Al	a Glu Thr. 325		Glu Me	t Glu Lys 330	Ala Ala	Val Arg 335	Leu
Gly Lys Le	eu Val Gly 340	Tyr Val	Ser Al	_	Val Glu	Tyr Leu 350	Tyr
Ser His As		Lys Phe	Tyr Ph 360	e Leu Glu	Leu Asn 365	Pro Arg	Leu
Gln Val GJ 370	u His Pro	Thr Thr 375		t Val Ser	Gly Val 380	Asn Leu	Pro
Ala Ala Gl 385	n Leu Glr	Ile Ala 390	Met Gl	y Ile Pro 395	Met His	Arg Ile	Ser 400
Asp Ile Ar	g Thr Leu 405		Met As:	n Pro His 410	Ser Ala	Ser Glu 415	Ile
Asp Phe Gl	u Phe Lys	Thr Gln	Asp Ala	a Thr Lys	Lys Gln	Arg Arg	Pro

420 425 430

Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro 435 440 445

Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe 450 455 460

Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly 465 470 475 480

Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe 485 490 495

Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys 500 505 510

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile 515 520 525

Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly 530 540

Trp Leu Asp Asp Leu Ile

<210> 47

<211> 540

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC FEATURE

<222> (1)..(540)

<223> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
 domain (AAs 22-561)

<400> 47

Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr 1 5 10 15

Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His
20 25 30

Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile 35 40 45

	50	·uı	Lys	Giu	110	55	DCI	Val	AIG	цуз	60	ALG	. IYI	GIU	1111
Phe 65	Gly	Asp	Asp	Arg	Thr 70	Val	Gln	Phe	Val	Ala 75	Met	Ala	Thr	Pro	Glu 80
Asp	Leu	Glu	Ala	Asn 85	Ala	Glu	Tyr	Ile	Arg 90	Met	Ala	Asp	Gln	Tyr 95	Ile
Glu	Val	Pro	Gly 100	Gly	Thr	Asn	Asn	Asn 105	Asn	Tyr	Ala	Asn	Val 110	Asp	Leu
Ile	Val	Asp 115	Ile	Ala	Glu	Arg	Ala 120	Asp	Val	Asp	Ala	Val 125	_	Ala	Gly
Trp	Gly 130	His	Ala	Ser	Glu	Asn 135	Pro	Leu	Leu	Pro	Glu 140	Lys	Leu	Ser	Gln
Ser 145	Lys	Arg	Lys	Val	Ile 150	Phe	Ile	Gly	Pro	Pro 155	Gly	Asn	Ala	Met	Arg 160
Ser	Leu	Gly	Asp	Lys 165	Ile	Ser	Ser	Thr	Ile 170	Val	Ala	Gln	Ser	Ala 175	Lys
Val	Pro	Cys	Ile 180	Pro	Trp	Ser	Gly	Thr 185	Gly	Val	Asp	Thr	Val 190	His	Val
Asp	Glu	Lys 195	Thr	Gly	Leu	Val	Ser 200	Val	Asp	Asp	Asp	Ile 205	Tyr	Gln	Lys
Gly	Cys 210	Cys	Thr	Ser	Pro	Glu 215	Asp	Gly	Leu	Gln	Lys 220	Ala	Lys	Arg	Ile
Gly 225	Phe	Pro	Val	Met	Ile 230	Lys	Ala	Ser	Glu	Gly 235	Gly	Gly	Gly	Lys	Gly 240
				Glu 245					250				_	255	
			260	Ile				265					270		
		275		His			280					285			
Thr	Asn	Ile	Ser	Leu	Phe	Gly	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg	His

295

290

Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr 305 310 315 320

300

Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly 325 330 335

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly 340 345 350

Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro 355 360 365

Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln 370 380

Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu 385 390 395 400

Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys 405 410 415

Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His
420 425 430

Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys
435
440
445

Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn 450 455 460

Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe 465 470 475 480

Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln 485 490 495

Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg 500 505 510

Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr 515 520 525

Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp 530 535 540

- <210> 48
- <211> 545
- <212> PRT
- <213> Phytophthora infestans
- <220>
- <221> MISC\_FEATURE
- <222> (1)..(545)
- <223> N-terminal deleted Phytophthora ACCase BC domain (AAs 11-555)
- <400> 48
- Asp Val Ala Ala Tyr Ala Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn 1 5 10 15
- Tyr Ala Ser Met Glu Glu Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro 20 25 30
- Ile Thr Ser Val Leu Ile Ala Asn Asn Gly Ile Ser Ala Val Lys Ala 35 40 45
- Ile Arg Ser Ile Arg Ser Trp Ser Tyr Glu Met Phe Ala Asp Glu His 50 55 60
- Val Val Thr Phe Val Val Met Ala Thr Pro Glu Asp Leu Lys Ala Asn 65 70 75 80
- Ala Glu Tyr Ile Arg Met Ala Glu His Val Val Glu Val Pro Gly Gly 85 90 95
- Ser Asn Asn His Asn Tyr Ala Asn Val Ser Leu Ile Ile Glu Ile Ala 100 105 110
- Glu Arg Phe Asn Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser 115 120 125
- Glu Asn Pro Leu Leu Pro Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile 130 135 140
- Val Phe Ile Gly Pro Pro Gly Lys Pro Met Arg Ala Leu Gly Asp Lys 145 150 155 160
- Ile Gly Ser Thr Ile Ile Ala Gln Ser Ala Lys Val Pro Thr Ile Ala 165 170 175
- Trp Asn Gly Asp Gly Met Glu Val Asp Tyr Lys Glu His Asp Gly Ile 180 185 190

Pro	Asp	Glu 195	ı Ile	: Tyr	` Asn	Ala	Ala 200		. Leu	a Arg	, Asp	Gly 205		n His	s Cys
Leu	. Asp 210		Cys	Lys	Arg	Ile 215		Phe	Pro	Val	. Met 220		. Lys	s Ala	ser
Glu 225	Gly	gly	Gly	· Gly	Lys 230	Gly	Ile	Arg	Met	Val 235		Glu	Glu	ı Ser	Gln 240
Val	Leu	. Ser	Ala	Trp 245	Glu	Ala	Val	Arg	Gly 250		Ile	Pro	Gly	Ser 255	Pro
Ile	Phe	Val	Met 260		Leu	Ala	Pro	Lys 265		Arg	His	Leu	Glu 270		Gln
Leu	Leu	Ala 275	Asp	Thr	Tyr	Gly	Asn 280	Ala	Ile	Ala	Leu	Ser 285	Gly	Arg	Asp
Cys	Ser 290	Val	Gln	Arg	Arg	His 295	Gln	Lys	Ile	Val	Glu 300	Glu	Gly	Pro	Val
Leu 305	Ala	Pro	Thr	Gln	Glu 310	Val	Trp	Glu	Lys	Met 315	Met	Arg	Ala	Ala	Thr 320
Arg	Leu	Ala	Gln	Glu 325	Val	Glu	Tyr	Val	Asn 330	Ala	Gly	Thr	Val	Glu 335	Tyr
Leu	Phe	Ser	Glu 340	Leu	Pro	Glu	Asp	Asn 345	Gly	Asn	Ser	Phe	Phe 350	Phe	Leu
Glu	Leu	Asn 355	Pro	Arg	Leu	Gln	Val 360	Glu	His	Pro	Val	Thr 365	Glu	Met	Ile
Thr	His 370	Val	Asn	Leu	Pro	Ala 375	Ala	Gln	Leu	Gln	Val 380	Ala	Met	Gly	Ile
Pro 385	Leu	His	Cys	Ile	Pro 390	Asp	Val	Arg	Arg	Leu 395	Tyr	Asn	Lys	Asp	Ala 400
Phe	Glu	Thr	Thr	Val 405	Ile	Asp	Phe	Asp	Ala 410	Glu	Lys	Gln	Lys	Pro 415	Pro
His	Gly		Val 420	Ile	Ala	Ala		Ile 425	Thr	Ala	Glu .		Pro 430	Asn	Ala

Gly Phe Gln Pro Thr Ser Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser 440 Thr Pro Asp Val Trp Gly Tyr Phe Ser Val Asp Ser Ser Gly Gln Val 455 His Glu Phe Ala Asp Ser Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg Lys Asn Met Val Leu Ala Leu Lys Glu Leu 490 Ser Ile Arg Gly Asp Ile His Thr Thr Val Glu Tyr Ile Val Asn Met 505 Met Glu Ser Asp Asp Phe Lys Tyr Asn Arg Ile Ser Thr Ser Trp Leu 520 Asp Glu Arg Ile Ser His His Asn Glu Val Arg Leu Gln Gly Arg Pro 535 Asp 545 <210> 49 <211> 535 <212> PRT <213> Phytophthora infestans <220> <221> MISC\_FEATURE (1)..(535) <223> N-terminal deleted Phytophthora ACCase BC domain (AAs 21-555) <400> 49 Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu Tyr Val Arg Leu 5 10 Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile Ala Asn Asn Gly 20 25 Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser Trp Ser Tyr Glu 35 40 45 Met Phe Ala Asp Glu His Val Val Thr Phe Val Val Met Ala Thr Pro

55

50

65 70 75 Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr Ala Asn Val Ser 85 90 Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Asp Thr Leu Ala 115 120 Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro Gly Lys Pro Met 130 135 Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile Ala Gln Ser Ala 150 Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met Glu Val Asp Tyr 165 Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn Ala Ala Met Leu 180 Arg Asp Gly Gln His Cys Leu Asp Glu Cys Lys Arg Ile Gly Phe Pro 195 Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Met Val His Glu Glu Ser Gln Val Leu Ser Ala Trp Glu Ala Val Arg Gly 225 235 Glu Ile Pro Gly Ser Pro Ile Phe Val Met Lys Leu Ala Pro Lys Ser 250 Arg His Leu Glu Val Gln Leu Leu Ala Asp Thr Tyr Gly Asn Ala Ile 265 Ala Leu Ser Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile 280 Val Glu Glu Pro Val Leu Ala Pro Thr Gln Glu Val Trp Glu Lys

Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met Ala Glu His Val

300

295

Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His 340 345 350

Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro Ala Ala Gln Leu 355 360 365

Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro Asp Val Arg Arg 370 375 380

Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile Asp Phe Asp Ala 385 390 395 400

Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala Ala Arg Ile Thr 405 410 415

Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser Gly Ala Ile Gln
420 425 430

Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly Tyr Phe Ser Val
435 440 445

Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser Gln Ile Gly His 450 455 460

Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg Lys Asn Met Val 465 470 475 480

Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile His Thr Thr Val 485 490 495

Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe Lys Tyr Asn Arg 500 505 510

Ile Ser Thr Ser Trp Leu Asp Glu Arg Ile Ser His His Asn Glu Val 515 520 525

Arg Leu Gln Gly Arg Pro Asp 530 535

<210> 50

- <211> 545
- <212> PRT
- <213> Phytophthora infestans
- <220>
- <221> MISC FEATURE
- <222> (1)..(545)
- <223> C-terminal deleted Phytophthora ACCase BC domain (AAs 1-545)
- <400> 50
- Met Val Ala Glu Glu Ala Pro Pro Ala Ala Asp Val Ala Ala Tyr Ala 1 5 10 15
- Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu 20 25 30
- Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile 35 40 45
- Ala Asn Asn Gly Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser 50 55 60
- Trp Ser Tyr Glu Met Phe Ala Asp Glu His Val Val Thr Phe Val Val 65 70 75 80
- Met Ala Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met 85 90 95
- Ala Glu His Val Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr
  100 105 110
- Ala Asn Val Ser Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp 115 120 125
- Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro 130 135 140
- Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro 145 150 155 160
- Gly Lys Pro Met Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile 165 170 175
- Ala Gln Ser Ala Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met 180 185 190
- Glu Val Asp Tyr Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn

195	200	205

Ala	Ala 210	Met	Leu	Arg	Asp	Gly 215	Gln	His	Суѕ	Leu	Asp 220	Glu	Cys	Lys	Arg
Ile 225	Gly	Phe	Pro	Val	Met 230	Ile	Lys	Ala	Ser	Glu 235	Gly	Gly	Gly	Gly	Lys 240
Gly	Ile	Arg	Met	Val 245	His	Glu	Glu	Ser	Gln 250	Val	Leu	Ser	Ala	Trp 255	Glu
Ala	Val	Arg	Gly 260	Glu	Ile	Pro	Gly	Ser 265	Pro	Ile	Phe	Val	Met 270	Lys	Leu
Ala	Pro	Lys 275	Ser	Arg	His	Leu	Glu 280	Val	Gln	Leu	Leu	Ala 285	Asp	Thr	Tyr
Gly	Asn 290	Ala	Ile	Ala	Leu	Ser 295	Gly	Arg	Asp	Cys	Ser 300	Val	Gln	Arg	Arg
His 305	Gln	Lys	Ile	Val	Glu 310	Glu	Gly	Pro	Val	Leu 315	Ala	Pro	Thr	Gln	Glu 320
Val	Trp	Glu	Lys	Met 325	Met	Arg	Ala	Ala	Thr 330	Arg	Leu	Ala	Gln	Glu 335	Val
Glu	Tyr	Val	Asn 340	Ala	Gly	Thr	Val	Glu 345	Tyr	Leu	Phe	Ser	Glu 350	Leu	Pro
Glu	Asp	Asn 355	Gly	Asn	Ser	Phe	Phe 360	Phe	Leu	Glu	Leu	Asn 365	Pro	Arg	Leu
Gln	Val 370	Glu	His	Pro	Val	Thr 375	Glu	Met	Ile	Thr	His 380	Val	Asn	Leu	Pro
Ala 385	Ala	Gln	Leu	Gln	Val 390	Ala	Met	Gly	Ile	Pro 395	Leu	His	Сув	Ile	Pro 400
Asp	Val	Arg	Arg	Leu 405	Tyr	Asn	Lys	Asp	Ala 410	Phe	Glu	Thr	Thr	Val 415	Ile
Asp	Phe	Asp	Ala 420	Glu	Lys	Gln	Lys	Pro 425	Pro	His	Gly	His	Val 430	Ile	Ala
Ala	Arg	Ile 435	Thr	Ala	Glu	Asp	Pro 440	Asn	Ala	Gly	Phe	Gln 445	Pro	Thr	Ser

Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly 455 Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser 470 475 Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg 485 490 Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile 505 His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe 520 Lys Tyr Asn Arg Ile Ser Thr Ser Trp Leu Asp Glu Arg Ile Ser His 535 His 545 <210> 51 <211> 535 <212> PRT <213> Phytophthora infestans <220> <221> MISC\_FEATURE <222> (1)..(535) <223> C-terminal deleted Phytophthora ACCase BC domain (AAs 1-535) <400> 51 Met Val Ala Glu Glu Ala Pro Pro Ala Ala Asp Val Ala Ala Tyr Ala Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu 20 25 Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile 40 35 Ala Asn Asn Gly Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser

Trp Ser Tyr Glu Met Phe Ala Asp Glu His Val Val Thr Phe Val Val

Met Ala Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met 90 Ala Glu His Val Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr 105 Ala Asn Val Ser Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp 120 Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro 135 Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro 150 155 Gly Lys Pro Met Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile 165 170 Ala Gln Ser Ala Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met 185 Glu Val Asp Tyr Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn 200 Ala Ala Met Leu Arg Asp Gly Gln His Cys Leu Asp Glu Cys Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Met Val His Glu Glu Ser Gln Val Leu Ser Ala Trp Glu Ala Val Arg Gly Glu Ile Pro Gly Ser Pro Ile Phe Val Met Lys Leu Ala Pro Lys Ser Arg His Leu Glu Val Gln Leu Leu Ala Asp Thr Tyr 275 Gly Asn Ala Ile Ala Leu Ser Gly Arg Asp Cys Ser Val Gln Arg Arg 290 His Gln Lys Ile Val Glu Glu Gly Pro Val Leu Ala Pro Thr Gln Glu 305

Val Trp Glu Lys Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val 330

Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro 345

Glu Asp Asn Gly Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu

Gln Val Glu His Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro

Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro 390

Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile 405 410

Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala 425

Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser 440

Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly 455 460

Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser 470

Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg 490

Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile

His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe 520

Lys Tyr Asn Arg Ile Ser Thr 530

<210> 52 <211> 581 <212> PRT

<213> Magnaporthe grisea

<220>

<221> MISC\_FEATURE

<222> (1)..(581)

<223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 12-592

<400> 52

Asn Ser Ser Arg Gln Arg Asn Gly Ala Asn Gly Val Thr Val Pro Val 1 5 10 15

Ala Asn Gly Lys Ala Thr Tyr Ala Gln Arg His Lys Ile Ala Asp His 20 25 30

Phe Ile Gly Gly Asn Arg Leu Glu Asn Ala Pro Pro Ser Lys Val Lys 35 40 45

Glu Trp Val Ala Ala His Asp Gly His Thr Val Ile Thr Asn Val Leu 50 55 60

Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg 65 70 75 80

Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr 85 90 95

Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg

Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr Asn Asn Asn Asn 115 120 125

Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu Arg Met Asn Val 130 135 140

His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu 145 150 155 160

Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro 165 170 175

Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile 180 185 190

Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp Ser Gly Thr Gly 195 200 205

Val	Asp 210	Ala	Val	Gln		Asp 215	Lys	Lys	Gly	Ile	Val ' 220	Thr	Val .	Asp	Asp	
Asp 225	Thr	Tyr	Ala	Lys	Gly 230	Cys	Val	Thr	Ser	Trp 235	Gln	Glu	Gly	Leu	Glu 240	
Lys	Ala	Arg	Gln	Ile 245	Gly	Phe	Pro	Val	Met 250	Ile	Lys	Ala	Ser	Glu 255	Gly	
Gly	Gly	Gly	Lys 260	Gly	Ile	Arg	Lys	Ala 265	Val	Ser	Glu	Glu	Gly 270	Phe	Glu	
Glu	Leu	Tyr 275		Ala	Ala	Ala	Ser 280	Glu	Ile	Pro	Gly	Ser 285	Pro	Ile	Phe	
Ile	Met 290		Lėu	Ala	Gly	Asn 295	Ala	Arg	His	Leu	Glu 300	Val	Gln	Leu	Leu	
Ala 305		Glr	ı Tyr	Gly	Asn 310	Asn	Ile	Ser	Leu	Phe 315	Gly	Arg	Asp	Cys	Ser 320	
Val	Gln	a Arg	J Arg	у Ніs 325		Lys	Ile	Ile	Glu 330	Glu	. Ala	Pro	Val	Thr 335	Ile	
Ala	Lys	s Pro	Asp 340		Phe	Lys	Ala	Met 345	Glu	Glu	ı Ala	Ala	Val 350	Arg	Leu	
Gly	y Arg	g Let 35		l Gly	Tyr	· Val	. Ser 360	Ala	Gly	Thr	· Val	Glu 365	Tyr	Leu	Tyr	
Se	r His		a Ası	o Ast	. Lys	375	e Tyr	Phe	e Leu	ı Glı	ı Leu 380	. Asn	Pro	Arg	Leu	
Gl: 38		l Gl	u Hi	s Pro	390		c Glu	ı Gly	y Val	. Sei 39!	r Gly 5	Val	. Asn	Leu	1 Pro 400	
Al	a Se	r Gl	n Le	u Glı 40!		e Ala	a Met	E Gly	7 Ile 410	e Pro	o Lev	ı His	arg	; Ile 415	e Ser	
As	p Il	e Ar	g Le 42		u Ty	r Gl	y Va	1 Ası 42	o Pro 5	o Ly	s Lei	ı Sei	t Thi 430	c Glu	ı Ile	
As	p Ph	ie As 43		ie Ly	s Ası	n Pr	o As 44		r Gl	u Ly	s Thi	c Gl: 44!	n Arg	g Ar	g Pro	
Se	er Pr	o Ly	ys Gl	y Hi	s Le	u Th	r Al	а Су	s Ar	g Il	e Th:	r Se	r Gl	u Asj	p Pro	

450 455 460

Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His Glu Leu Asn Phe 465 470 475 480

Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly
485 490 495

Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Tyr 500 505 510

Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val Ile Ala Leu Lys 515 520 525

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile 530 535 540

Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly 545 550 555

Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr Ala Glu Arg Pro Asp 565 570 575

Lys Met Leu Ala Val 580

<210> 53

<211> 571

<212> PRT

<213> Magnaporthe grisea

<220>

<221> MISC FEATURE

<222> (1)..(571)

<223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 22-591)

<400> 53

Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr Tyr Ala Gln Arg 1 5 10 15

His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg Leu Glu Asn Ala 20 25 30

Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His Asp Gly His Thr 35 40 45

Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys

Glu	Ile	Arg	Ser	Val	Arg	Lys	Trp	Ala	Tyr	Glu	Thr	Phe	Gly	Asp	Glu	
65					70					75					80	

60

55

50

Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala 85 90 95

Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly
100 105 110

Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val 115 120 125

Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala 130 135 140

Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys 145 150 155 160

Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp 165 170 175

Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile 180 185 190

Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly
195 200 205

Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser 210 215 220

Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met 225 230 235 240

Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys Ala Val \$245\$ \$250\$ \$255

Ser Glu Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile 260 265 270

Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His 275 280 285

Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu 290 295 300

Phe 305	Gly	Arg	Asp	Cys	Ser 310	Val	Gln	Arg	Arg	His 315	Gln	Lys	Ile	Ile	Glu 320
Glu	Ala	Pro	Val	Thr 325	Ile	Ala	Lys	Pro	Asp 330	Thr	Phe	Lys	Ala	Met 335	Glu
Glu	Ala	Ala	Val 340	Arg	Leu	Gly	Arg	Leu 345	Val	Gly	Tyr	Val	Ser 350	Ala	Gly
Thr	Val	Glu 355	Tyr	Leu	Tyr	Ser	His 360	Ala	Asp	Asp	Lys	Phe 365	Tyr	Phe	Leu
Glu	Leu 370	Asn	Pro	Arg	Leu	Gln 375	Val	Glu	His	Pro	Thr 380	Thr	Glu	Gly	Val
Ser 385	Gly	Val	Asn	Leu	Pro 390	Ala	Ser	Gln	Leu	Gln 395	Ile	Ala	Met	Gly	Ile 400
Pro	Leu	His	Arg	Ile 405	Ser	Asp	Ile	Arg	Leu 410	Leu	Tyr	Gly	Val	Asp 415	Pro
Lys	Leu	Ser	Thr 420	Glu	Ile	Asp	Phe	Asp 425	Phe	Lys	Asn	Pro	Asp 430	Ser	Glu
Lys	Thr	Gln 435	Arg	Arg	Pro	Ser	Pro 440	Lys	Gly	His	Leu	Thr 445	Ala	Cys	Arg
Ile	Thr 450	Ser	Glu	Asp	Pro	Gly 455	Glu	Gly	Phe	Lys	Pro 460	Ser	Asn	Gly	Val
Met 465	His	Glu	Leu	Asn	Phe 470	Arg	Ser	Ser	Ser	Asn 475	Val	Trp	Gly	Tyr	Phe 480
Ser	Val	Gly	Thr	Gln 485	Gly	Gly	Ile	His	Ser 490	Phe	Ser	Asp	Ser	Gln 495	Phe
Gly	His	Ile	Phe 500	Ala	Tyr	Gly	Glu	Asn 505	Arg	Ser	Ala	Ser	Arg 510	Lys	His
Met	Val	Ile 515	Ala	Leu	Lys	Glu	Leu 520	Ser	Ile	Arg	Gly	Asp 525	Phe	Arg	Thr
Thr	Val 530	Glu	Tyr	Leu	Ile	Lys 535	Leu	Leu	Glu	Thr	Glu 540	Ala	Phe	Glu	Glu

Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Leu 545 550 555 560

Thr Ala Glu Arg Pro Asp Lys Met Leu Ala Val 565 570

<210> 54

<211> 581

<212> PRT

<213> Magnaporthe grisea

<220>

<221> MISC\_FEATURE

<222> (1)..(581)

<223> C-terminal deleted Magnaporthe ACCase (AAs 2-582)

<400> 54

Thr Glu Thr Asn Gly Thr Ala Ala Ala Ala Asn Ser Ser Arg Gln Arg 1 5 10 15

Asn Gly Ala Asn Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr 20 25 30

Tyr Ala Gln Arg His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg 35 40 45

Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His 50 55 60

Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile 65 70 75 80

Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr 85 90 95

Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu 100 105 110

Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val

Glu Val Pro Gly Gly Thr Asn Asn Asn Tyr Ala Asn Val Glu Leu 130 135 140

Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly 145 150 155 160

165 170 Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg 180 185 Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln 200 Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile 215 210 Asp Lys Lys Gly Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly 235 230 Cys Val Thr Ser Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly 250 245 Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile 265 Arg Lys Ala Val Ser Glu Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn 310 315 Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln 330 Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Pro Asp Thr Phe 345 Lys Ala Met Glu Glu Ala Ala Val Arg Leu Gly Arg Leu Val Gly Tyr 360 Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys 375 Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr 390 395

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala

Thr Glu Gly Val Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile 410 Ala Met Gly Ile Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr 425 Gly Val Asp Pro Lys Leu Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn 440 Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu 455 Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro 470 475 Ser Asn Gly Val Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val 485 490 Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu 545 550 555 Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile 565 570 Ser Lys Lys Leu Thr 580 <210> 55 <211> 571 <212> PRT <213> Magnaporthe grisea <220> <221> MISC\_FEATURE <222> (1)..(571) <223> C-terminal deleted Magnaporthe ACCase BC domain (AAs 2-572)

<400> 55

Thr Glu Thr Asn Gly Thr Ala Ala Ala Ala Asn Ser Ser Arg Gln Arg 1 5 10 15

Asn Gly Ala Asn Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr 20 25 30

Tyr Ala Gln Arg His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg 35 40 45

Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His 50 55

Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile 65 70 75 80

Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr 85 90 95

Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu 100 105 110

Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val 115 120 125

Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu 130 140

Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly
145 150 155 160

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala 165 170 175

Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg 180 185 190

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln 195 200 205

Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile 210 215 220

Asp Lys Lys Gly Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly 225 230 235 235

Cys Val Thr Ser Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly

245	250	255

Phe Pro Val	Met Ile	Lys Ala Ser	Gin Già Già	Gly Gly Lys (	Hy Ile
	260		265	270	

- Arg Lys Ala Val Ser Glu Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala 275 280 285
- Ala Ser Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly 290 295 300
- Asn Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn 305 310 315 320
- Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln 325 330 335
- Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Pro Asp Thr Phe 340 345 350
- Lys Ala Met Glu Glu Ala Ala Val Arg Leu Gly Arg Leu Val Gly Tyr 355 360 365
- Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys 370 375 380
- Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr 385 390 395 400
- Thr Glu Gly Val Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile 405 410 415
- Ala Met Gly Ile Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr 420 425 430
- Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu 450 455 460
- Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro 465 470 475 480
- Ser Asn Gly Val Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val \$485\$

Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser 500 Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala 515 520 Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly 530 Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu 555 Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly Trp 565 570 <210> 56 <211> 622 <212> PRT <213> Homo sapiens <220> <221> MISC\_FEATURE <222> (1)..(622) <223> C-terminal deleted Human ACCasel BC domain (AAs 1-622) <400> 56 Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser 40 Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile 55 Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser 70 Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser 90

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe
100 105 110

Gly	Gly	Asn 115	Lys	Val	Ile	Glu	Lys 120	Val	Leu	Ile	Ala	Asn 125	Asn	Gly	Ile
Ala	Ala 130	Val	Lys	Cys	Met	Arg 135	Ser	Ile	Arg	Arg	Trp 140	Ser	Tyr	Glu	Met
Phe 145	Arg	Asn	Glu	Arg	Ala 150	Ile	Arg	Phe	Val	Val 155	Met	Val	Thr	Pro	Glu 160
Asp	Leu	Lys	Ala	Asn 165	Ala	Glu	Tyr	Ile	Lys 170	Met	Ala	Asp	His	Tyr 175	Val
Pro	Val	Pro	Gly 180		Pro	Asn	Asn	Asn 185	Asn	Tyr	Ala	Asn	Val 190	Glu	Leu
Ile	Leu	Asp 195		Ala	Lys	Arg	Ile 200	Pro	Val	Gln	Ala	Val 205	Trp	Ala	Gly
Trp	Gly 210		s Ala	Ser	Glu	Asn 215	Pro	Lys	Leu	Pro	Glu 220	Leu	Leu	Leu	Lys
Asn 225		r Ile	e Ala	ı Phe	Met 230	Gly	Pro	Pro	Ser	Glr 235	n Ala	. Met	. Trp	) Ala	Leu 240
Gly	As <u>r</u>	Ly.	s Ile	e Ala 245		Ser	: Ile	· Val	Ala 250	a Glr	1 Thi	Ala	a Gly	7 Ile 255	e Pro
Thi	. Le	ı Pr	o Trj 26		c Gly	seı	g Gly	Let 26!	ı Arç	y Val	l Ası	o Tr	9 Glr 270	ı Glu	ı Asn
Ası	o Ph		r Ly	s Arg	g Ile	e Lev	ı Asr 280	n Va:	l Pro	o Gli	n Gl	u Let 28!	и Тут 5	r Glu	ı Lys
Gl	у Ту 29		ıl Ly	s As	p Val	l As <sub>]</sub>		, Gl	y Le	u Ly	s Al 30	a Al	a Gl	u Gl	u Val
G1 <sup>.</sup>		r Pı	o Va	l Me	t Ile 31	e Ly 0	s Ala	a Se	r Gl	u Gl 31	y Gl 5	y Gl	y Gl	у Lу	s Gly 320
Il	e Ar	g Ly	ys Va	ıl As 32		n Al	a Asj	p As	р Ph 33	e Pr 0	o As	n Le	u Ph	e Ar 33	g Glr 5
Va	ıl Gl	n A	la Gl 34		ıl Pr	o Gl	y Se	r Pr 34	o Il	.e Ph	ne Va	ıl Me	t Ar 35	g Le	u Ala

Lys Gln Se:		Leu Glu	Val 360	Gln	Ile	Leu	Ala	Asp 365	Gln	Tyr	Gly
Asn Ala Ilo 370	e Ser Leu	Phe Gly 375		Asp	Cys	Ser	Val 380	Gln	Arg	Arg	His
Gln Lys Il	e Ile Glu	Glu Ala 390	Pro	Ala	Thr	Ile 395	Ala	Thr	Pro	Ala	Val 400
Phe Glu Hi	s Met Glu 405	-	Ala	Val	Lys 410	Leu	Ala	Lys	Met	Val 415	Gly
Tyr Val Se	r Ala Gly 420	Thr Val	Glu	Tyr 425	Leu	Tyr	Ser	Gln	Asp 430	Gly	Ser
Phe Tyr Ph 43		Leu Asr	Pro 440	Arg	Leu	Gln	Val	Glu 445	His	Pro	Cys
Thr Glu Me 450	t Val Ala	Asp Val		Leu	Pro	Ala	Ala 460	Gln	Leu	Gln	Ile
Ala Met Gl	y Ile Pro	Leu Tyr 470	Arg	Ile	Lys	Asp 475	Ile	Arg	Met	Met	Tyr 480
Gly Val Se	r Pro Trp 485		Ser	Pro	Ile 490	Asp	Phe	Glu	Asp	Ser 495	Ala
His Val Pr	o Cys Pro 500	Arg Gly	His	Val 505	Ile	Ala	Ala	Arg	Ile 510	Thr	Ser
Glu Asn Pr 51	_	Gly Phe	Lys 520	Pro	Ser	Ser	Gly	Thr 525	Val	Gln	Glu
Leu Asn Ph 530	e Arg Ser	Asn Lys		Val	Trp	Gly	Tyr 540	Phe	Ser	Val	Ala
Ala Ala Gl 545	y Gly Leu	His Glu 550	. Phe	Ala	Asp	Ser 555	Gln	Phe	Gly	His	Cys 560
Phe Ser Tr	p Gly Glu 565	_	g Glu	Glu	Ala 570	Ile	Ser	Asn	Met	Val 575	Val
Ala Leu Ly	s Glu Leu 580	Ser Ile	. Arg	Gly 585	Asp	Phe	Arg	Thr	Thr 590	Val	Glu

Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile 595 600 605

Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln 610 615 620

<210> 57

<211> 612

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (1)..(612)

<223> C-terminal deleted Human ACCase1 BC domain (AAs 1-612)

<400> 57

Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His 1 5 10 15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu 20 25 30

Ile Ser Asn Leu Val Lys Leu Asp Leu Glu Glu Lys Glu Gly Ser
35 40 45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile 50 55 60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser 65 70 75 80

Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser 85 90 95

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe
100 105 110

Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile 115 120 125

Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met 130 135 140

Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu 145 150 155 160

- Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val 165 170 175
- Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu 180 185 190
- Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly
  195 200 205
- Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Lys 210 215 220
- Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu 225 230 235 240
- Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro 245 250 255
- Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn 260 265 270
- Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys 275 280 285
- Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val 290 295 300
- Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly 305 310 315
- Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln 325 330 335
- Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala 340 345 350
- Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly 355 360 365
- Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His 370 380
- Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val 385 390 395 400
- Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser 420 425 430

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys
435
440
445

Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile 450 455 460

Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr 465 470 480

Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala 485 490 495

His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser 500 505 510

Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu 515 520 525

Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala 530 540

Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys 545 550 555 560

Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val 565 570 575

Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu 580 585 590

Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile 595 600 605

Asp Thr Gly Trp 610

<210> 58

<211> 522

<212> PRT

<213> Homo sapiens

<220>

<221> MISC FEATURE

<222> (2)..(632)

<223> N- and C-terminal deleted Human ACCase1 (AAs 102-622)

<400> 58

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys

1 10 15

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys 20 25 30

Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu 35 40 45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala 50 55 60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly 65 70 75 80

Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile 85 90 95

Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala 115 120 125

Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile 130 135 140

Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp 145 150 155 160

Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys 165 170 175

Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys 180 185 190

Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val

Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Val 210 215 220

Asn Asn Ala 225	Asp Asp	Phe Pro 230	Asn 1	Leu Phe	e Arg 235	Gln	Val	Gln	Ala	Glu 240
Val Pro Gly	Ser Pro 245	Ile Phe	Val 1	Met Arg 250	-	Ala	Lys	Gln	Ser 255	Arg
His Leu Glu	Val Gln 260	Ile Leu		Asp Gli 265	n Tyr	Gly	Asn	Ala 270	Ile	Ser
Leu Phe Gly 275		Cys Ser	Val (	Gln Ar	g Arg		Gln 285	Lys	Ile	Ile
Glu Glu Ala 290	Pro Ala	Thr Ile 295		Thr Pro		Val 300	Phe	Glu	His	Met
Glu Gln Cys 305	Ala Val	Lys Leu 310	Ala i	Lys Me	t Val 315	Gly	Tyr	Val	Ser	Ala 320
Gly Thr Val	Glu Tyr 325	_	Ser (	Gln As <sub>l</sub>	_	Ser	Phe	Tyr	Phe 335	Leu
Glu Leu Asr	Pro Arg	Leu Gln		Glu Hi: 345	s Pro	Сув	Thr	Glu 350	Met	Val
Ala Asp Val		Pro Ala	Ala (	Gln Le	ı Gln	Ile	Ala 365	Met	Gly	Ile
Pro Leu Tyr 370	Arg Ile	Lys Asp 375		Arg Me		Tyr 380	Gly	Val	Ser	Pro
Trp Gly Asp 385	Ser Pro	Ile Asp 390	Phe (	Glu As <sub>l</sub>	9 Ser 395	Ala	His	Val	Pro	Cys 400
Pro Arg Gly	His Val 405		Ala	Arg Ile 41		Ser	Glu	Asn	Pro 415	Asp
Glu Gly Phe	Lys Pro 420	Ser Ser	_	Thr Vai	l Gln	Glu	Leu	Asn 430	Phe	Arg
Ser Asn Lys 435		Trp Gly	Tyr :	Phe Se	r Val		Ala 445	Ala	Gly	Gly
Leu His Glu 450	Phe Ala	Asp Ser		Phe Gl	-	Cys 460	Phe	Ser	Trp	Gly

Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu 470 Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 490 Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp 505 Leu Asp Arg Leu Ile Ala Glu Lys Val Gln 515 520 <210> 59 <211> 512 <212> PRT <213> Homo sapiens <220> <221> MISC\_FEATURE <222> (2)..(512)
<223> N- and C-terminal deleted Human ACCase1 BC domain (AAs 102-512) <400> 59 Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys 5 10 Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys 2.0 Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu 40 35 Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala 50 Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala 100

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Lys Asn Gly Ile Ala

120

Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala Lys Gln Ser Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Ala Thr Ile Ala Thr Pro Ala Val Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile

Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile

Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr Gly Val Ser Pro 370 375 Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala His Val Pro Cys 390 395 400 Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp 405 410 415 Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg 420 425 Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Ala Gly Gly 435 440 445 Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly 450 455 Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 485 Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp 500 505 <210> 60 <211> 764 <212> PRT <213> Homo sapiens <220> <221> MISC\_FEATURE <222> (1)..(764) <223> C-terminal deleted Human ACCase2 BC domain (AAs 1-764) <400> 60 Met Val Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile 25

Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe

Pro Ala Ser 50	Asp Asn	Ser Gly 55	Glu T	Thr Pro	Gln Arg 60	Asn	Gly	Glu	Gly
His Thr Leu 65	Pro Lys	Thr Pro	Ser G	Sln Ala	Glu Pro 75	Ala	Ser	His	Lys 80
Gly Pro Lys	Asp Ala 85	Gly Arg	Arg A	Arg Asn 90	Ser Leu	Pro	Pro	Ser 95	His
Gln Lys Pro	Pro Arg 100	Asn Pro		Ser Ser 105	Ser Asp	Ala	Ala 110	Pro	Ser
Pro Glu Leu 115	Gln Ala	Asn Gly	Thr G	Hy Thr	Gln Gly	Leu 125	Glu	Ala	Thr
Asp Thr Asn 130	Gly Leu	Šer Ser 135		Ala Arg	Pro Gln 140	Gly	Gln	Gln	Ala
Gly Ser Pro 145	Ser Lys	Glu Asp 150	Lys I	Lys Gln	Ala Asn 155	Ile	Lys	Arg	Gln 160
Leu Met Thr	Asn Phe 165	Ile Leu	Gly S	Ser Phe 170	Asp Asp	Tyr	Ser	Ser 175	Asp
Glu Asp Ser	Val Ala 180	Gly Ser		Arg Glu 185	Ser Thr	Arg	Lys 190	Gly	Ser
Arg Ala Ser 195	Leu Gly	Ala Leu	Ser I 200	Leu Glu	Ala Tyr	Leu 205	Thr	Thr	Gly
Glu Ala Glu 210	Thr Arg	Val Pro 215		Met Arg	Pro Ser 220	Met	Ser	Gly	Leu
His Leu Val 225	Lys Arg	Gly Arg 230	Glu H	His Lys	Lys Leu 235	Asp	Leu	His	Arg 240
Asp Phe Thr	Val Ala 245	Ser Pro	Ala G	Flu Phe 250	Val Thr	Arg	Phe	Gly 255	Gly
Asp Arg Val	Ile Glu 260	Lys Val		Ile Ala 265	Asn Asn	Gly	Ile 270	Ala	Ala
Val Lys Cys 275	Met Arg	Ser Ile	Arg A 280	Arg Trp	Ala Tyr	Glu 285	Met	Phe	Arg
Asn Glu Arg	Ala Ile	Arg Phe	Val V	/al Met	Val Thr	Pro	Glu	Asp	Leu

290 295 300

Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val 305 310 315 320

Pro Gly Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val 325 330 335

Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly 340 345 350

His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly 355

Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp 370 375 380

Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu 385 390 395 400

Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu 405 410 415

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly 420 425 430

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly 435 440 445

Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile 450 455 460

Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val 465 470 475 480

Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln 485 490 495

His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn 500 505 510

Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln 515 520 525

Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe 530 540

Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val <210> 61

<211> 754 <212> PRT

- <213> Homo sapiens
- <220>
- <221> MISC\_FEATURE
- <222> (1) ... (754)
- <223> C-terminal deleted Human ACCase2 BC domain (AAs 1-754)
- <400> 61
- Met Val Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr
- Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile 25 20
- Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe
- Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly 50
- His Thr Leu Pro Lys Thr Pro Ser Gln Ala Glu Pro Ala Ser His Lys 70 75 65
- Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His 90 85
- Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser 100
- Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr 125 115
- Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala 140 130
- Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln 155 150 145
- Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp
- Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser 190 180
- Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly 200 195

His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu 

Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly 

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly 

Phe	Pro 450	Leu	Met	Ile	Lys	Ala 455	Ser	Glu	Gly	Gly	Gly 460	Gly	Lys	Gly	Ile
Arg 465	Lys	Ala	Glu	Ser	Ala 470	Glu	Asp	Phe	Pro	Ile 475	Leu	Phe	Arg	Gln	Val 480
Gln	Ser	Glu	Ile	Pro 485	Gly	Ser	Pro	Ile	Phe 490	Leu	Met	Lys	Leu	Ala 495	Gln
His	Ala	Arg	His 500	Leu	Glu	Val	Gln	Ile 505	Leu	Ala	Asp	Gln	Tyr 510	Gly	Asn
Ala	Val	Ser 515	Leu	Phe	Gly	Arg	Asp 520	Cys	Ser	Ile	Gln	Arg 525	Arg	His	Gln
Lys	Ile 530		Glu	Glu	Ala	Pro 535		Thr	Ile	Ala	Pro 540	Leu	Ala	Ile	Phe
Glu 545		Met	Glu	Gln	Cys 550		Ile	Arg	Leu	Ala 555	Lys	Thr	Val	Gly	Tyr 560
Val	Ser	Ala	ı Gly	Thr 565		Glu	туг	Leu	Tyr 570	Ser	Gln	Asp	Gly	Ser 575	Phe
His	: Phe	e Lev	ı Glu 580		ı Asn	Pro	Arg	Leu 585	. Gln	Val	Glu	His	Pro 590	Cys	Thr
Glu	ı Met	: Ile 59!		ı Asp	val	. Asr	Leu 600	Pro	) Ala	. Ala	Gln	Leu 605	Gln	Ile	Ala
Met	610		l Pro				g Leu			) Ile	e Arg 620	Leu	. Leu	Tyr	Gly
Gl:		r Pr	o Tr <u>ı</u>	o Gly	y Vai 630		r Pro	o Ile	e Sei	635	e Glu	Thr	Pro	Ser	Asn 640
Pr	o Pr	o Le	u Ala	a Arg		y Hi	s Val	L Il€	e Ala 650	a Ala	a Arg	, Ile	e Thi	Ser 655	Glu
As	n Pr	o As	p Gl 66		y Ph	e Ly	s Pro	o Se: 66!	r Se: 5	r Gly	y Thr	r Val	L Gl: 670	n Glu O	ı Leu
As	n Ph	e Ar	g Se	r Se	r Ly	s As	n Va	l Tr	p Gl	у Ту	r Phe	e Sei	r Vai	l Ala	a Ala

Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe

695

Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala 715 710

700

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr 730

Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp 745

Thr Gly

690

<210> 62

<211> 522

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (2)..(522)

<223> N- and C-terminal Human ACCase2 BC domain (AAs 224-764)

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg 10

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys 25 20

Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu 35 40

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala 50

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly

Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile

Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala 100

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala

115 120 125

Phe	Leu	Gly	Pro	Pro	Ser	Glu	Ala	Met	$\mathtt{Trp}$	Ala	Leu	GIY	Asp	гàг	тте
	130	_				135					140				

- Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg
  145 150 155 160
- Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln 165 170 175
- Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val 180 185 190
- Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly Phe Pro 195 200 205
- Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys 210 215 220
- Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser 225 230 235 240
- Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala 245 250 255
- Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val 260 265 270
- Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile 275 280 285
- Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe 290 295 300
- Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser 305 310 315 320
- Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe 325 330 335
- Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met 340 345 350
- Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly 355 360 365

Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser 375 370 Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro 395 390 Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro 405 410 Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe 425 420 Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly 445 435 440 Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp 455 460 450 Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys 470 475 480 465 Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile 490 485 Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly 505 500 Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val 515 520 <210> 63 <211> 512 <212> PRT <213> Homo sapiens <220> <221> MIC FEATURE <222> (2)..(512) <223> N- and C-terminal deleted Human ACCase2 BC domain (AAs 224-754) <400> 63 Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg 10 Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys

25

Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu 40 Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly 75 70 Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile 85 Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala 105 Ser Glu Asn Pro Lys Leu Pro Glu Leu Cys Lys Asn Gly Val Ala 120 Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile 135 130 Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg 155 150 145 Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln 170 Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val 185 Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly Phe Pro

Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys 210 220

200

195

Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser 225 230 235 240

Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala 245 250 255

Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val 260 265 270

- Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile 275 280 285
- Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe 290 295 300
- Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser 305 310 315
- Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe 325 330 335
- Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met
- Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly 355 360 365
- Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser 370 380
- Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro 385 390 395 400
- Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro 405 410 415
- Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe 420 425 430
- Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly 435 440 445
- Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp
- Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys 465 470 475 480
- Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile 485 490 495
- Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly 500 505 510

<210> 64 <211> 521 <212> PRT <213> Magnaporthe grisea <220> <221> MISC\_FEATURE <222> (1)..(521) <223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 72-592) <400> 64 Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr 50 Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu 70 Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu 85 90 Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile 100 105 Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile 120 Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp

Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val 145 150 155 160

135

Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln 165 170 175

Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys 180 185 190

Ala	Ser	Glu 195	Gly	Gly	Gly	Gly	Lys 200	Gly	Ile	Arg	Lys	Ala 205	Val	Ser	Glu
Glu	Gly 210	Phe	Glu	Glu	Leu	Tyr 215	Lys	Ala	Ala	Ala	Ser 220	Glu	Ile	Pro	Gly
Ser 225	Pro	Ile	Phe	Ile	Met 230	Lys	Leu	Ala	Gly	Asn 235	Ala	Arg	His	Leu	Glu 240
Val	Gln	Leu	Leu	Ala 245	Asp	Gln	Tyr	Gly	Asn 250	Asn	Ile	Ser	Leu	Phe 255	Gly
Arg	Asp	Cys	Ser 260	Val	Gln	Arg	Arg	His 265	Gln	Lys	Ile	Ile	Glu 270	Glu	Ala
Pro	Val	Thr 275	Ile	Ala	Lys	Pro	Asp 280	Thr	Phe	Lys	Ala	Met 285	Glu	Glu	Ala
Ala	Val 290	Arg	Leu	Gly	Arg	Leu 295	Val	Gly	Tyr	Val	Ser 300	Ala	Gly	Thr	Val
Glu 305	Tyr	Leu	Tyr	Ser	His 310	Ala	Asp	Asp	Lys	Phe 315	Tyr	Phe	Leu	Glu	Leu 320
Asn	Pro	Arg	Leu	Gln 325	Val	Glu	His	Pro	Thr 330	Thr	Glu	Gly	Val	Ser 335	Gly
Val	Asn	Leu	Pro 340	Ala	Ser	Gln	Leu	Gln 345	Ile	Ala	Met	Gly	Ile 350	Pro	Leu
His	Arg	Ile 355	Ser	Asp	Ile	Arg	Leu 360	Leu	Tyr	Gly	Val	Asp 365	Pro	Lys	Leu
Ser	Thr 370	Glu	Ile	Asp	Phe	Asp 375	Phe	Lys	Asn	Pro	Asp 380	Ser	Glu	Lys	Thr
Gln 385	Arg	Arg	Pro	Ser	Pro 390	Lys	Gly	His	Leu	Thr 395	Ala	Cys	Arg	Ile	Thr 400
Ser	Glu	Asp	Pro	Gly 405	Glu	Gly	Phe	Lys	Pro 410	Ser	Asn	Gly	Val	Met 415	His
Glu	Leu	Asn	Phe 420	Arg	Ser	Ser	Ser	Asn 425	Val	Trp	Gly	Tyr	Phe 430	Ser	Val
G1 v	Thr	Gln	Glv	Glv	Tle	His	Ser	Phe	Ser	Asp	Ser	Gln	Phe	Glv	His

435 440 445

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val 450 455 460

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val 465 470 475 480

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr 485 490 495

Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr Ala 500 505 510

Glu Arg Pro Asp Lys Met Leu Ala Val 515 520

<210> 65

<211> 511

<212> PRT

<213> Magnaporthe grisea

<220>

<221> MISC\_FEATURE

<222> (1)..(511)

<223> N- and C-terminal deleted Magnaporthe ACCase BC domain (AAs 72-582)

<400> 65

Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile 1 5 10 15

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala 20 25 30

Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala 35 40 45

Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr 50 55 60

Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu 65 70 75 80

Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu
85 90 95

Asn	Pro	Lys	Leu 100	Pro	Glu	Ser	Leu	Ala 105	Ala	Ser	Pro	Lys	Lys 110	Ile	Ile
Phe	Ile	Gly 115	Pro	Pro	Gly	Ser	Ala 120	Met	Arg	Ser	Leu	Gly 125	Asp	Lys	Ile
Ser	Ser 130	Thr	Ile	Val	Ala	Gln 135	His	Ala	Gln	Val	Pro 140	Cys	Ile	Pro	Trp
Ser 145	Gly	Thr	Gly	Val	Asp 150	Ala	Val	Gln	Ile	Asp 155	Lys	Lys	Gly	Ile	Val 160
Thr	Val	Asp	Asp	Asp 165	Thr	Tyr	Ala	Lys	Gly 170	Cys	Val	Thr	Ser	Trp 175	Gln
Glu	Gly	Leu	Glu 180	Lys	Ala	Arg	Gln	Ile 185	Gly	Phe	Pro	Val	Met 190	Ile	Lys
Ala	Ser	Glu 195	Gly	Gly	Gly	Gly	Lys 200	Gly	Ile	Arg	Lys	Ala 205	Val	Ser	Glu
Glu	Gly 210	Phe	Glu	Glu	Leu	Tyr 215	Lys	Ala	Ala	Ala	Ser 220	Glu	Ile	Pro	Gly
Ser 225	Pro	Ile	Phe	Ile	Met 230	Lys	Leu	Ala	Gly	Asn 235	Ala	Arg	His	Leu	Glu 240
Val	Gln	Leu	Leu	Ala 245	Asp	Gln	Tyr	Gly	Asn 250	Asn	Ile	Ser	Leu	Phe 255	Gly
Arg	Asp	Cys	Ser 260	Val	Gln	Arg	Arg	His 265	Gln	Lys	Ile	Ile	Glu 270	Glu	Ala
Pro	Val	Thr 275	Ile	Ala	Lys	Pro	Asp 280	Thr	Phe	Lys	Ala	Met 285	Glu	Glu	Ala
Ala	Val 290	Arg	Leu	Gly	Arg	Leu 295	Val	Gly	Tyr	Val	Ser 300	Ala	Gly	Thr	Val
Glu 305	Tyr	Leu	Tyr	Ser	His 310	Ala	Asp	Asp	Lys	Phe 315	Tyr	Phe	Leu	Glu	Leu 320
Asn	Pro	Arg	Leu	Gln 325	Val	Glu	His	Pro	Thr 330	Thr	Glu	Gly	Val	Ser 335	Gly
Val	Asn	Leu	Pro	Ala	Ser	Gln	Leu	Gln	Ile	Ala	Met	Gly	Ile	Pro	Leu

340 345 350

His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu 355 360 365

Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr 370 375 380

Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr 385 390 395 400

Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His
405 410 415

Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val 420 425 430

Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His 435 440 445

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val 450 455 460

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val 465 470 475 480

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr 485 490 495

Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr 500 505 510

<210> 66

<211> 501

<212> PRT

<213> Magnaporthe grisea

<220>

<221> misc feature

<223> N- and C-terminal deleted Magnaporthe ACCase BC domain (AAs
72-572)

<400> 66

Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile
1 5 10 15

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala

Ile	Gln	Phe	Thr	Val	Met	Ala	Thr	Pro	Glu	Asp	Leu	Gln	Ala	Asn	Ala
		35					40					45			

- Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr 50 60
- Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu 65 70 75 80
- Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu 85 90 95
- Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile 100 105 110
- Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile 115 120 125
- Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp 130 135 140
- Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val 145 150 155 160
- Thr Val Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln 165 170 175
- Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys 180 185 190
- Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys Ala Val Ser Glu
  195 200 205
- Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly 210 215 220
- Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu 225 230 235 240
- Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu Phe Gly 245 250 255
- Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala 260 265 270

Pro	Val	Thr 275	Ile	Ala	Lys	Pro	Asp 280	Thr	Phe	Lys	Ala	Met 285	Glu	Glu	Ala
Ala	Val 290	Arg	Leu	Gly	Arg	Leu 295	Val	Gly	Tyr	Val	Ser 300	Ala	Gly	Thr	Val
Glu 305	Tyr	Leu	Tyr	Ser	His 310	Ala	Asp	Asp	Lys	Phe 315	Tyr	Phe	Leu	Glu	Leu 320
Asn	Pro	Arg	Leu	Gln 325	Val	Glu	His	Pro	Thr 330	Thr	Glu	Gly	Val	Ser 335	Gly
Val	Asn	Leu	Pro 340	Ala	Ser	Gln	Leu	Gln 345	Ile	Ala	Met	Gly	Ile 350	Pro	Leu
His	Arg	Ile 355	Ser	Asp	Ile	Arg	Leu 360	Leu	Tyr	Gly	Val	Asp 365	Pro	Lys	Leu
	370				Phe	375					380				
385					Pro 390					395					400
				405					410					415	
			420		Ser			425					430		
_		435			·Ile		440					445			
	450				Glu	455					460				
465					Leu 470					475					480
Glu	Tyr	Leu	ı Ile	485	Leu	. Leu	Glu	Thr	Glu 490		Phe	: Glu	i GLu	Asn 495	Thr

Ile Thr Thr Gly Trp 500

- <210> 67
- <211> 491
- <212> PRT
- <213> Magnaporthe grisea
- <220>
- <221> MISC\_FEATURE
- <222> (1)..(491)
- <223> N- and C-terminal deleted ACCase BC domain (AAs 72-562)
- <400> 67
- Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile 1 5 10 15
- Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala 20 25 30
- Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala 35 40 45
- Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr 50 55 60
- Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu 65 70 75 80
- Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu 85 90 95
- Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile 100 105 110
- Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile 115 120 125
- Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp 130 135 140
- Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val 145 150 155 160
- Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln 165 170 175
- Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys 180 185 190

Ala	Ser	Glu 195	Gly	Gly	Gly	Gly	Lys 200	Gly	Ile	Arg	Lys	Ala 205	Val	Ser	Glu
Glu	Gly 210	Phe	Glu	Glu	Leu	Tyr 215	Lys	Ala	Ala	Ala	Ser 220	Glu	Ile	Pro	Gly
Ser 225	Pro	Ile	Phe	Ile	Met 230	Lys	Leu	Ala	Gly	Asn 235	Ala	Arg	His	Leu	Glu 240
Val	Gln	Leu	Leu	Ala 245	Asp	Gln	Tyr	Gly	Asn 250	Asn	Ile	Ser	Leu	Phe 255	Gly
Arg	Asp	Cys	Ser 260	Val	Gln	Arg	Arg	His 265	Gln	Lys	Ile	Ile	Glu 270	Glu	Ala
Pro	Val	Thr 275	Ile	Ala	Lys	Pro	Asp 280	Thr	Phe	Lys	Ala	Met 285	Glu	Glu	Ala
Ala	Val 290	Arg	Leu	Gly	Arg	Leu 295	Val	Gly	Tyr	Val	Ser 300	Ala	Gly	Thr	Val
Glu 305	Tyr	Leu	Tyr	Ser	His 310	Ala	Asp	Asp	Lys	Phe 315	Tyr	Phe	Leu	Glu	Leu 320
Asn	Pro	Arg	Leu	Gln 325	Val	Glu	His	Pro	Thr 330	Thr	Glu	Gly	Val	Ser 335	Gly
Val	Asn	Leu	Pro 340	Ala	Ser	Gln	Leu	Gln 345	Ile	Ala	Met	Gly	Ile 350	Pro	Leu
His	Arg	Ile 355	Ser	Asp	Ile	Arg	Leu 360	Leu	Tyr	Gly	Val	Asp 365	Pro	Lys	Leu
Ser	Thr 370	Glu	Ile	Asp	Phe	Asp 375	Phe	Lys	Asn	Pro	Asp 380	Ser	Glu	Lys	Thr
Gln 385	Arg	Arg	Pro	Ser	Pro 390	Lys	Gly	His	Leu	Thr 395	Ala	Суз	Arg	Ile	Thr 400
Ser	Glu	Asp	Pro	Gly 405	Glu	Gly	Phe	Lys	Pro 410	Ser	Asn	Gly	Val	Met 415	His
Glu	Leu	Asn	Phe 420	Arg	Ser	Ser	Ser	Asn 425	Val	Trp	Gly	Tyr	Phe 430	Ser	Val

Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His 440

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val 455

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val 475 465

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala 485

<210> 68

<211> 525

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC\_FEATURE
<222> (1)..(525)
<223> N-terminal deleted Yeast ACCase BC domain (AAs--57-581)

<400> 68

Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp 25

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu 40

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro

Gly Gly Thr Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp 70

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg 105

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly 120 125 115

Asp	Lys 130	Ile	Ser	Ser	Thr	Ile 135	Val	Ala	Gln	Ser	Ala 140	Lys	Val	Pro	Cys
Ile 145	Pro	Trp	Ser	Gly	Thr 150	Gly	Val	Asp	Thr	Val 155	His	Val	Asp	Glu	Lys 160
Thr	Gly	Leu	Val	Ser 165	Val	Asp	Asp	Asp	Ile 170	Tyr	Gln	Lys	Gly	Cys 175	Cys
Thr	Ser	Pro	Glu 180	Asp	Gly	Leu	Gln	Lys 185	Ala	Lys	Arg	Ile	Gly 190	Phe	Pro
Val	Met	Ile 195	Lys	Ala	Ser	Glu	Gly 200	Gly	Gly	Gly	Lys	Gly 205	Ile	Arg	Gln
Val	Glu 210	Arg	Glu	Glu	Asp	Phe 215	Ile	Ala	Leu	Tyr	His 220	Gln	Ala	Ala	Asn
Glu 225	Ile	Pro	Gly	Ser	Pro 230	Ile	Phe	Ile	Met	Lys 235	Leu	Ala	Gly	Arg	Ala 240
Arg	His	Leu	Glu	Val 245	Gln	Leu	Leu	Ala	Asp 250	Gln	Tyr	Gly	Thr	Asn 255	Ile
Ser	Leu	Phe	Gly 260	Arg	Asp	Cys	Ser	Val 265	Gln	Arg	Arg	His	Gln 270	Lys	Ile
Ile	Glu	Glu 275	Ala	Pro	Val	Thr	Ile 280	Ala	Lys	Ala	Glu	Thr 285	Phe	His	Glu
Met	Glu 290	_	Ala			_	Leu	_	_	Leu	Val 300	_	Tyr	Val	Ser
Ala 305	Gly	Thr	Val	Glu	Tyr 310	Leu	Tyr	Ser	His	Asp 315	Asp	Gly	Lys	Phe	Tyr 320
Phe	Leu	Glu	Leu	Asn 325	Pro	Arg	Leu	Gln	Val 330	Glu	His	Pro	Thr	Thr 335	Glu
Met	Val	Ser	Gly 340	Val	Asn	Leu	Pro	Ala 345	Ala	Gln	Leu	Gln	Ile 350	Ala	Met
Gly	Ile	Pro 355	Met	His	Arg	Ile	Ser 360	Asp	Ile	Arg	Thr	Leu 365	Tyr	Gly	Met
Asn	Pro	His	Ser	Ala	Ser	Glu	Ile	Asp	Phe	Glu	Phe	Lys	Thr	Gln	Asp

370 375 380

Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala 385 390 395 400

Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly 405 410 415

Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly
420 425 430

Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser 435 440 445

Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg 450 455 460

Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe 465 470 475 480

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe
485 490 495

Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His
500 505 510

Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val 515 520 525

<210> 69

<211> 515

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC\_FEATURE

<222> (1)..(515)

<223> N- and C-terminal deleted Yeast ACCase BC domain (AAs 57-571)

<400> 69

Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val 1 5 10 15

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp 20 25 30

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu

40

35

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro 50 55 60

45

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp 65 70 75 80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His 85 90 95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg 100 105 110

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly 115 120 125

Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys 130 135 140

Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys
145 150 155 160

Thr Gly Leu Val Ser Val Asp Asp Ile Tyr Gln Lys Gly Cys Cys 165 170 175

Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro 180 185 190

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Gln 195 200 205

Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn 210 215 220

Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala 225 230 235 240

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile 245 250 255

Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile 260 265 270

Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu 275 280 285

Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His

Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser

Lys Met Thr 515

- <210> 70
- <211> 505
- <212> PRT
- <213> Saccharomyces cerevisiae
- <220>
- <221> MISC\_FEATURE
- <222> (1)..(505)
- <223> N- and C-terminal deleted Yeast ACCase BC domain (AAs 57-561)
- <400> 70
- Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val 1 5 10 15
- Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp 20 25 30
- Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu
  35 40 45
- Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro 50 60
- Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp 65 70 75 80
- Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His
  85 90 95
- Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg
  100 105 110
- Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly 115 120 125
- Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys 130 135 140
- Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys
  145 150 155 160
- Thr Gly Leu Val Ser Val Asp Asp Ile Tyr Gln Lys Gly Cys Cys 165 170 175
- Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro 180 185 190

Val	Met	Ile 195	Lys	Ala	Ser	Glu	Gly 200	Gly	Gly	Gly	Lys	Gly 205	Ile	Arg	Gln
Val	Glu 210	Arg	Glu	Glu	Asp	Phe 215	Ile	Ala	Leu	Tyr	His 220	Gln	Ala	Ala	Asn
Glu 225	Ile	Pro	Gly	Ser	Pro 230	Ile	Phe	Ile	Met	Lys 235	Leu	Ala	Gly	Arg	Ala 240
Arg	His	Leu	Glu	Val 245	Gln	Leu	Leu	Ala	Asp 250	Gln	Tyr	Gly	Thr	Asn 255	Ile
Ser	Leu	Phe	Gly 260	Arg	qaA	Cys	Ser	Val 265	Gln	Arg	Arg	His	Gln 270	Lys	Ile
Ile	Glu	Glu 275	Ala	Pro	Val	Thr	Ile 280	Ala	Lys	Ala	Glu	Thr 285	Phe	His	Glu
Met	Glu 290	Lys	Ala	Ala	Val	Arg 295	Leu	Gly	Lys	Leu	Val 300	Gly	Tyr	Val	Ser
Ala 305	Gly	Thr	Val	Glu	Туг 310		Tyr	Ser	His	Asp 315		Gly	Lys	Phe	Tyr 320
Phe	Leu	Glu	Leu	Asn 325	Pro	Arg	Leu	Gln	Val 330		His	Pro	Thr	Thr 335	
Met	Val	Ser	Gly 340		Asn	Leu	Pro	Ala 345		Gln	Leu	Gln	Ile 350	Ala	Met
Gly	Ile	Pro 355		His	Arg	Ile	Ser 360		Ile	Arg	Thr	Leu 365		Gly	Met
Asn	Pro 370		Ser	Ala	Ser	Glu 375		Asp	Phe	: Glu	380		Thr	Gln	Asp
Ala 385		Lys	Lys	Gln	Arg 390		Pro	) Ile	Pro	395		His	Cys	Thr	Ala 400
Cys	Arg	Ile	. Thr	Ser 405	Glu	Asp	Pro	Asn	Asp 410		Phe	. Lys	Pro	Ser 415	
Gly	Thr	Leu	His 420		ı Lev	ı Asr	n Ph∈	425		Ser	Ser	Asn	Val 430		Gly

Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser 440 435 Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg 460 455 Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe 470 475 465 Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe 490 485 Glu Asp Asn Thr Ile Thr Thr Gly Trp 505 500 <210> 71 <211> 495 <212> PRT <213> Saccharomyces cerevisiae <220> <221> MISC\_FEATURE <222> (1)..(495) <223> N- and C-terminal deleted YEast ACCase BC domain (AAs 57-551) <400> 71 Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp 25 Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu 35 Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro 55 50 Gly Gly Thr Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp 65 70 Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His 85 90

110

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg 105

пур	Val	115		ııe	GIY	Pro	120		Asn	ı Ala	Met	125		Leu	ı Gly
Asp	Lys 130		Ser	Ser	Thr	Ile 135		Ala	Gln	Ser	Ala 140		Val	Pro	Cys
Ile 145		Trp	Ser	Gly	Thr 150	Gly	Val	Asp	Thr	Val 155		Val	Asp	Glu	Lys 160
Thr	Gly	Leu	. Val	Ser 165	Val	Asp	Asp	Asp	Ile 170		Gln	Lys	Gly	Cys 175	Cys
Thr	Ser	Pro	Glu 180		Gly	Leu	Gln	Lys 185	Ala	Lys	Arg	Ile	Gly 190	Phe	Pro
Val	Met	Ile 195		Āla	Ser	Glu	Gly 200	Gly	Gly	Gly	Lys	Gly 205	Ile	Arg	Gľn
Val	Glu 210	Arg	Glu	Glu	Asp	Phe 215	Ile	Ala	Leu	Tyr	His 220	Gln	Ala	Ala	Asn
Glu 225	Ile	Pro	Gly	Ser	Pro 230	Ile	Phe	Ile	Met	Lys 235	Leu	Ala	Gly	Arg	Ala 240
Arg	His	Leu	Glu	Val 245	Gln	Leu	Leu	Ala	Asp 250	Gln	Tyr	Gly	Thr	Asn 255	Ile
Ser	Leu	Phe	Gly 260	Arg	Asp	Cys	Ser	Val 265	Gln	Arg	Arg	His	Gln 270	Lys	Ile
Ile	Glu	Glu 275	Ala	Pro	Val	Thr	Ile 280	Ala	Lys	Ala	Glu	Thr 285	Phe	His	Glu
Met	Glu 290	Lys	Ala	Ala	Val	Arg 295	Leu	Gly	Lys	Leu	Val 300	Gly	Tyr	Val	Ser
Ala 305	Gly	Thr	Val	Glu	Tyr 310	Leu	Tyr	Ser	His	Asp 315	Asp	Gly	Lys	Phe	Tyr 320
Phe	Leu	Glu	Leu	Asn 325	Pro	Arg	Leu	Gln	Val 330	Glu	His	Pro	Thr	Thr 335	Glu
Met	Val	Ser	Gly 340	Val	Asn	Leu	Pro	Ala 345	Ala	Gln	Leu	Gln	Ile 350	Ala	Met
Glv	Ile	Pro	Met	His	Ara	Tle	Ser	Asp	Tle	Δrα	Thr	T.e.11	ጥንረም	G1 v	Mot

Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp 370 375 380

- Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala 385 390 395 400
- Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly 405 410 415
- Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly
  420 425 430
- Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser 435 440 445
- Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg 450 455 460
- Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe 465 470 475 480
- Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp 485 490 490